

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 16:04:25 ; Search time 39 Seconds

(without alignments)
577.301 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

Sequence: 1 MHLPEDMENALTGSQSSHA.....EAGSEAEKQDSEKPLLEL 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR 79:*

2: Pirl:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664	55.6	445	2 I38027	MLN 64 protein - h
2	204	17.1	478	2 T16170	hypothetical prote
3	102.5	8.6	348	2 H90281	hypothetical prote
4	93.5	7.8	424	2 D75080	glucose-1-phosphat
5	90	7.5	1911	2 T43048	calcium channel al
6	86.5	7.2	767	2 T21969	hypothetical prote
7	85.5	7.2	396	2 B81299	probable molybdopt
8	85.5	7.2	438	2 A57219	Batten disease-rel
9	85	7.1	448	2 G70172	conserved hypothet
10	84.5	7.1	471	2 A41680	integral membrane
11	83.5	7.0	352	2 H97002	probable integral
12	83	6.9	291	2 AE0302	sugar ABC transpor
13	83	6.9	590	1 S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2 B29835	Tras protein - Esc
15	82.5	6.9	239	1 C64227	hypothetical prote
16	82.5	6.9	341	2 S51265	probable N-acetylgl
17	82.5	6.9	406	2 T43120	conserved hypothet
18	82.5	6.9	891	2 T37397	major core protein
19	82	6.9	589	2 T52070	RNAL protein homol
20	82	6.9	589	2 A36983	RNAL homolog fug1
21	82	6.9	1466	2 T30566	ATP-binding caset
22	81	6.8	385	2 B84447	hypothetical prote
23	81	6.8	529	2 T23190	hypothetical prote
24	81	6.8	532	2 S46831	probable membrane
25	80.5	6.7	156	2 I84498	melatonin receptor
26	80.5	6.7	322	2 T45568	hypothetical prote
27	80.5	6.7	396	2 T50229	probable transmemb
28	80.5	6.7	417	2 C44038	tryptophan permeas
29	80.5	6.7	463	2 AE1155	amino acid transpo

probable integral
membrane
membrane protein t
major core protein
major core protein
probable glucan sy
conserved hypothet
hypothetical prote
RTM1 protein - yea
hypothetical prote
probable SNF2 subf
amino acid transpo
immediate-early pr
hypothetical prote
spermidine/putresc
rnfD protein homol
serotonin receptor
IB3/5-polypeptide
cdd2 protein - Clo
hypothetical prote
stage III sporulat
undecaprenyl-phosp
ABC transporter (p
hypothetical prote
hypothetical prote
spermidine/putresc
probable membrane
conserved hypothet
ABC transporter (p
NADH2 dehydrogenas
A11L protein - var
NADH2 dehydrogenas
sodium- and chlori
probable colanic b
NADH2 dehydrogenas
A10L protein - var
hypothetical prote
sodium channel pro
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
multidrug resistan
hypothetical prote
hypothetical prote
probable tail fibre
phage tail protein
probable sugar ABC
hypothetical prote
probable membrane
potassium channel
probable iron-upta
hypothetical trans
NADH2 dehydrogenas
hypothetical prote
hypothetical prote
hypothetical prote
cystic fibrosis tr
protein C48A7.1 [i
melatonin receptor
hypothetical prote
hypothetical prote
conserved hypothet
probable membrane
hypothetical prote
hypothetical prote
low affinity trypt
low affinity trypt
tryptophan transpo
5-hydroxytryptamin
NADH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistan	176	72.5	6.1	325	2	H86670	hypothetical prote
104	75.5	6.3	708	2	T29669	hypothetical prote	177	72.5	6.1	336	2	C88951	protein C383.2 [i
105	75.5	6.3	775	2	T52107	anion channel prot	178	72.5	6.1	389	2	A55493	oxytocin receptor
106	75.5	6.3	1142	2	T39103	probable negative	179	72.5	6.1	428	2	AF0173	probable paraquat-
107	75	6.3	249	2	G64470	sulfate/thiosulfat	180	72.5	6.1	499	2	AF0173	virulence factor M
108	75	6.3	274	2	A82509	probable phosphati	181	72.5	6.1	513	2	H70453	pituitary adenylat
109	75	6.3	330	2	B71163	probable oligopept	182	72.5	6.1	522	2	S47631	hypothetical prote
110	75	6.3	473	2	A38627	gamma-aminobutyric	183	72.5	6.1	635	2	T29705	hypothetical prote
111	75	6.3	526	2	T45950	hypothetical prote	184	72.5	6.1	718	2	T23465	probable transloca
112	75	6.3	649	2	C69810	anion-binding prot	185	72.5	6.1	749	2	S57913	probable cap-bindi
113	75	6.3	753	2	H90124	hypothetical prote	186	72.5	6.1	1539	2	C94508	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase	187	72	6.0	279	2	T30037	hypothetical prote
115	74.5	6.2	276	2	A95881	probable trehalase	188	72	6.0	306	2	T21099	hypothetical prote
116	74.5	6.2	335	2	H72420	oligopeptide ABC t	189	72	6.0	339	2	AE1156	probable permease
117	74.5	6.2	355	2	JC4304	orphan G protein-c	190	72	6.0	377	2	G97199	hypothetical prote
118	74.5	6.2	471	2	A34863	serotonin receptor	191	72	6.0	379	2	T27805	ubiquinol-cytochro
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter	192	72	6.0	415	1	T11349	late L1 52K protei
120	74.5	6.2	500	2	T14826	transcription init	193	72	6.0	415	1	WNAD52	late L1 52K protei
121	74.5	6.2	574	2	T05364	probable low-affin	194	72	6.0	453	2	WNAD52	glycosyl hydrolase
122	74.5	6.2	618	1	S38004	hypothetical prote	195	72	6.0	453	2	D89760	conserved hypothet
123	74.5	6.2	1808	2	T47792	hypothetical prote	196	72	6.0	479	2	S64587	probable cytochrom
124	74	6.2	231	1	C69540	cobalamin (5'-phos	197	72	6.0	497	2	G96611	hypothetical prote
125	74	6.2	231	1	B69422	quinone-reactive N	198	72	6.0	514	2	T15338	hypothetical prote
126	74	6.2	281	1	S26018	NADH2 dehydrogenas	199	72	6.0	594	2	T42660	hypothetical prote
127	74	6.2	286	2	S73424	permidine/putresc	200	72	6.0	600	2	T39873	hypothetical prote
128	74	6.2	312	2	C72547	probable aspartate	201	72	6.0	630	2	T07966	probable ethylene
129	74	6.2	312	2	H86732	hypothetical prote	202	72	6.0	1038	2	S37854	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto	203	72	6.0	1094	2	S22573	DNA-directed DNA p
131	74	6.2	350	2	T38848	Mel-1a melatonin r	204	72	6.0	1113	2	T20140	hypothetical prote
132	74	6.2	396	2	H89869	hypothetical prote	205	72	6.0	1220	2	T18291	patched protein -
133	74	6.2	442	2	C86859	transmembrane effl	206	72	6.0	1275	2	JU0092	trp protein - frui
134	74	6.2	449	2	S02011	serotonin receptor	207	72	6.0	1282	2	T30804	p-glycoprotein 6 -
135	74	6.2	475	2	T36317	probable amino aci	208	71.5	6.0	210	2	S52050	cytochrome-c oxida
136	74	6.2	485	2	T24115	hypothetical prote	209	71.5	6.0	225	1	MMIH68	E1 membrane glycop
137	74	6.2	487	1	C71417	cytochrome P450 di	210	71.5	6.0	237	2	H70975	hypothetical prote
138	74	6.2	493	2	JC7378	L-lysine 6-aminotr	211	71.5	6.0	246	2	AG3644	flagellar biosynth
139	74	6.2	1123	2	T51517	telomerase reverse	212	71.5	6.0	301	2	F86647	hypothetical prote
140	73.5	6.2	153	2	E95845	conserved hypothet	213	71.5	6.0	341	2	F90084	hypothetical prote
141	73.5	6.2	192	2	A84727	hypothetical prote	214	71.5	6.0	345	2	T33706	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote	215	71.5	6.0	348	2	AB3516	RnB-related prote
143	73.5	6.2	318	2	S76712	hypothetical prote	216	71.5	6.0	355	2	AB3516	sensory transducti
144	73.5	6.2	338	2	T40448	conserved hypothet	217	71.5	6.0	362	2	S48689	prostaglandin E(2)
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro	218	71.5	6.0	366	2	S51280	EP3-alpha receptor
146	73.5	6.2	384	2	AF0636	glucans biosynthes	219	71.5	6.0	366	2	I45469	Mel-1a melatonin r
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro	220	71.5	6.0	381	2	T11776	ubiquinol-cytochro
148	73.5	6.2	385	2	A69844	ABC transporter (A	221	71.5	6.0	383	2	T38194	hypothetical prote
149	73.5	6.2	413	2	AD1738	Similar to multidr	222	71.5	6.0	386	1	S34043	oxytocin receptor
150	73.5	6.2	442	2	C96672	hypothetical prote	223	71.5	6.0	390	2	S66497	isotocin receptor
151	73.5	6.2	491	1	EDBEM5	immediate-early pr	224	71.5	6.0	435	2	AD1340	maltodextrin ABC-t
152	73.5	6.2	634	2	F82623	potassium uptake p	225	71.5	6.0	435	2	AB1711	125K surface antig
153	73.5	6.2	637	2	H83945	DNA mismatch repai	226	71.5	6.0	471	2	PS0154	hexose transport p
154	73.5	6.2	640	2	B32935	hypothetical prote	227	71.5	6.0	510	2	T10124	hypothetical prote
155	73.5	6.2	731	2	T31914	hypothetical prote	228	71.5	6.0	524	2	T02499	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept	229	71.5	6.0	603	2	H90061	hypothetical prote
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p	230	71.5	6.0	651	2	T46050	bet7 protein homol
158	73	6.1	114	2	F71925	cag island protein	231	71.5	6.0	669	2	D64137	mediates transport
159	73	6.1	282	2	S26030	NADH2 dehydrogenas	232	71.5	6.0	670	2	A49580	hypothetical prote
160	73	6.1	339	2	T15560	hypothetical prote	233	71.5	6.0	823	2	T34472	adenylate cyclase
161	73	6.1	450	1	WBEM4	49-2K membrane pro	234	71.5	6.0	1407	2	B42239	genome polyprotein
162	73	6.1	453	2	T30985	hypothetical prote	235	71.5	6.0	3010	1	S18030	cag pathogenicity
163	73	6.1	553	2	A71823	hypothetical prote	236	71	5.9	114	2	H64586	E1 membrane glycop
164	73	6.1	788	2	G89901	hypothetical prote	237	71	5.9	225	1	MMIHAI	conserved hypothet
165	73	6.1	971	2	T00268	hypothetical prote	238	71	5.9	250	2	A82367	probable processin
166	73	6.1	1075	2	B96508	hypothetical prote	239	71	5.9	258	2	A81355	chlorophyll a/b-bi
167	73	6.1	6805	2	S20901	hypothetical prote	240	71	5.9	280	2	S33443	hypothetical prote
168	72.5	6.1	209	2	S72929	probable transport	241	71	5.9	339	2	T16745	NADH2 dehydrogenas
169	72.5	6.1	222	2	B85866	probable transport	242	71	5.9	345	2	T12372	hypothetical prote
170	72.5	6.1	222	2	B91022	hypothetical prote	243	71	5.9	345	2	T25561	hypothetical prote
171	72.5	6.1	222	2	H64996	ubiquinol-cytochro	244	71	5.9	361	2	C90603	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro	245	71	5.9	361	2	F86759	hypothetical prote
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi	246	71	5.9	416	2	B87286	3-deoxy-D-manno-oc
174	72.5	6.1	304	2	A86696	conserved hypothet	247	71	5.9	423	2	AF1335	transcription regu
175	72.5	6.1	315	2	H86598	protein P20N2.8 [i	248	71	5.9	471	2	A43956	serotonin receptor

249	71	5.9	546	2	S48932	hypothetical prote	322	69.5	5.8	285	2	P70194	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip	323	69.5	5.8	321	2	S59388	probable membrane
251	71	5.9	576	2	T22509	hypothetical prote	324	69.5	5.8	339	2	A97736	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type	325	69.5	5.8	347	2	G90444	hypothetical prote
253	253	5.9	676	2	E59725	hypothetical prote	326	69.5	5.8	354	2	I58186	probable G protein
254	71	5.9	788	2	E71813	probable component	327	69.5	5.8	361	2	A53216	prostaglandin E2 r
255	71	5.9	913	2	T52485	neurofilament prot	328	69.5	5.8	362	2	S36766	prostaglandin E re
256	71	5.9	2437	2	T18482	hypothetical prote	329	69.5	5.8	384	2	S62758	ubiquinol-cytochro
257	70.5	5.9	203	1	T31684	probable bacitraci	330	69.5	5.8	385	2	S36765	prostaglandin E re
258	70.5	5.9	266	2	H98208	probable permease	331	69.5	5.8	387	2	S36767	prostaglandin E re
259	70.5	5.9	266	2	A13077	hypothetical prote	332	69.5	5.8	394	2	T32561	hypothetical prote
260	70.5	5.9	266	2	T41414	probable receptor-	333	69.5	5.8	400	2	AG1208	cell-division prot
261	70.5	5.9	279	2	AH2408	permease protein o	334	69.5	5.8	402	2	S51791	Drosophila translo
262	70.5	5.9	291	2	S22041	hypothetical prote	335	69.5	5.8	405	2	E90986	probable colanic a
263	70.5	5.9	340	2	S76294	hypothetical prote	336	69.5	5.8	405	2	H85831	probable colanic a
264	70.5	5.9	352	2	B90537	hypothetical prote	337	69.5	5.8	405	2	G64971	Putative colanic a
265	70.5	5.9	365	2	I38748	prostaglandin recep	338	69.5	5.8	411	2	B53216	prostaglandin E2 r
266	70.5	5.9	365	2	S51315	prostaglandin E re	339	69.5	5.8	417	2	S36764	prostaglandin E re
267	70.5	5.9	374	2	I38747	prostaglandin recep	340	69.5	5.8	421	2	G72300	conserved hypotet
268	70.5	5.9	374	2	S51317	prostaglandin E re	341	69.5	5.8	436	2	T44832	probable emulsan r
269	70.5	5.9	388	2	S51316	prostaglandin E re	342	69.5	5.8	453	2	D98003	conserved hypotet
270	70.5	5.9	388	2	I38750	prostaglandin recep	343	69.5	5.8	477	2	T25798	hypothetical prote
271	70.5	5.9	389	2	S71336	mesotocin receptor	344	69.5	5.8	490	2	E82740	C4-dicarboxylate t
272	70.5	5.9	390	2	S43375	prostaglandin E re	345	69.5	5.8	503	2	C86250	hypothetical prote
273	70.5	5.9	390	2	S51313	prostaglandin E re	346	69.5	5.8	507	2	T50054	probable transport
274	70.5	5.9	393	2	S51318	prostaglandin E re	347	69.5	5.8	515	2	E86534	ADP/ATP translocas
275	70.5	5.9	423	1	E71065	hypothetical prote	348	69.5	5.8	547	2	G86581	integral membrane
276	70.5	5.9	425	2	S51319	prostaglandin E re	349	69.5	5.8	547	2	T72042	organic cation tra
277	70.5	5.9	472	2	AG3600	cellulose synthase	350	69.5	5.8	557	2	JW0089	ABC transporter AT
278	70.5	5.9	496	2	B64638	conserved hypotet	351	69.5	5.8	557	2	AC2137	hypothetical prote
279	70.5	5.9	521	2	E64181	probable cytochrom	352	69.5	5.8	570	2	D96776	mismatch repair pr
280	70.5	5.9	548	2	A81650	conserved hypotet	353	69.5	5.8	577	2	D97337	DNA polymerase III
281	70.5	5.9	556	2	T16790	hypothetical prote	354	69.5	5.8	579	2	AG1412	DNA polymerase III
282	70.5	5.9	574	2	S45754	probable membrane	355	69.5	5.8	579	2	AF1788	gamma-aminobutyric
283	70.5	5.9	598	2	F46027	gamma-aminobutyric	356	69.5	5.8	599	2	S11073	hypothetical prote
284	70.5	5.9	599	1	ACRTGT	probable serine/th	357	69.5	5.8	604	2	T11042	hypothetical prote
285	70.5	5.9	700	2	T10566	hypothetical prote	358	69.5	5.8	607	2	F84525	Mutator-like trans
286	70.5	5.9	766	2	T48463	chitin synthase (E	359	69.5	5.8	616	2	E84463	Mutator-like trans
287	70.5	5.9	1026	2	T18220	hypothetical prote	360	69.5	5.8	877	2	S58824	probable membrane
288	70.5	5.9	1583	2	F97846	hypothetical prote	361	69.5	5.8	881	2	S46633	probable membrane
289	70.5	5.9	1787	2	T20160	hypothetical prote	362	69.5	5.8	1704	2	A59188	ATP-binding caset
290	70.5	5.9	5138	2	B96695	hypothetical prote	363	69.5	5.8	1704	2	S71363	probable ATP-bindi
291	70	5.9	189	2	T51847	manganese-binding	364	69.5	5.8	1778	2	UT0382	apolipoprotein B -
292	291	5.9	199	2	T08902	hypothetical prote	365	69.5	5.8	2629	2	I46569	apolipoprotein B -
293	70	5.9	213	2	F86310	protein Flk3.8 [im	366	69.5	5.8	7829	2	T15789	hypothetical prote
294	70	5.9	256	2	T13597	hypothetical prote	367	69	5.8	1639	2	E83941	hypothetical prote
295	295	5.9	287	2	T52317	chlorophyll a/b-bi	368	69	5.8	195	2	A96998	CDP-diglyceride sy
296	70	5.9	292	2	H64244	H+-transporting tw	369	69	5.8	244	2	H96934	uncharacterized me
297	70	5.9	307	2	E95010	ABC transporter, p	370	69	5.8	256	2	C64145	hypothetical prote
298	70	5.9	307	2	B97882	hypothetical prote	371	69	5.8	261	2	T07481	hypothetical prote
299	70	5.9	330	2	T30981	hypothetical prote	372	69	5.8	273	2	F83805	hypothetical prote
300	70	5.9	333	2	I38974	G protein-coupled	373	69	5.8	273	2	C71707	hypothetical prote
301	70	5.9	371	2	T46421	hypothetical prote	374	69	5.8	289	2	S72554	melatonin receptor
302	70	5.9	388	2	A55597	oxytocin receptor	375	69	5.8	291	2	D96002	probable sugar upt
303	70	5.9	416	2	A85112	probable ankyrin-r	376	69	5.8	300	2	T32702	hypothetical prote
304	70	5.9	418	2	T08982	proline/betaine tr	377	69	5.8	338	2	A99979	hypothetical prote
305	70	5.9	420	2	E72357	sugar ABC transpor	378	69	5.8	339	2	B69436	LSU ribosomal prot
306	70	5.9	427	2	T01905	hypothetical prote	379	69	5.8	345	2	AH1514	hypothetical prote
307	70	5.9	437	2	C91261	glutamate-aspartat	380	69	5.8	351	2	AD0273	probable integral
308	70	5.9	437	2	G86101	glutamate-aspartat	381	69	5.8	379	2	S58447	ubiquinol-cytochro
309	70	5.9	438	2	AF3215	ABC transporter, m	382	69	5.8	382	2	AI3175	conserved hypotet
310	70	5.9	450	2	T42595	envelope protein 5	383	69	5.8	383	2	D71424	hypothetical prote
311	70	5.9	494	2	B89827	hypothetical prote	384	69	5.8	388	2	I69644	O-antigen polymera
312	70	5.9	532	2	T49467	related to COP1-in	385	69	5.8	436	2	T11268	NADH2 dehydrogenas
313	70	5.9	551	2	A87019	probable cytochrom	386	69	5.8	437	2	A42384	glutamate-aspartat
314	70	5.9	554	2	T27878	hypothetical prote	387	69	5.8	443	2	T19512	hypothetical prote
315	70	5.9	558	2	H72565	hypothetical prote	388	69	5.8	478	2	S25821	transposase - Bac1
316	70	5.9	675	2	T22323	hypothetical prote	389	69	5.8	478	2	T33985	hypothetical prote
317	70	5.9	735	2	S46830	urea transport pro	390	69	5.8	508	2	E96804	probable thioedox
318	70	5.9	963	2	T26022	hypothetical prote	391	69	5.8	523	2	T11916	NADH2 dehydrogenas
319	70	5.9	1930	2	F86200	protein Fl2K11.17	392	69	5.8	540	2	T24675	hypothetical prote
320	69.5	5.8	133	1	MNIHHC	nonstructural prot	393	69	5.8	549	2	E70784	cytochrome b homol
321	69.5	5.8	206	2	S76279	hypothetical prote	394	69	5.8	579	2	A64100	inner membrane cop

395	69	5.8	599	2	G90476	probable Na+/H+ an	468	68	5.7	426	2	C59831	conserved hypothet
396	69	5.8	600	2	T11889	NADH2 dehydrogenas	469	68	5.7	464	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H95592	probable multispan	470	68	5.7	473	2	H71044	hypothetical prote
398	69	5.8	659	2	D84633	probable multispan	471	68	5.7	475	2	E83450	cytochrome-c oxida
399	69	5.8	791	2	T12455	hypothetical prote	472	68	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	potassium channel	473	68	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84490	hypothetical prote	474	68	5.7	477	2	C85095	hypothetical 52.1
402	69	5.8	933	2	AD3309	hypothetical membr	475	68	5.7	488	2	A53572	prostaglandin E2 r
403	69	5.8	1058	2	T30580	p-type ATPase - sl	476	68	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	68	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	68	5.7	542	2	A69261	probable ABC-trans
406	69	5.8	1515	2	T04204	hypothetical prote	479	68	5.7	542	2	B81910	ABC transporter, A
407	69	5.8	3010	1	A45573	genome polyprotein	480	68	5.7	542	2	E81105	hypothetical prote
408	68.5	5.7	225	2	AE0371	probable carboxype	481	68	5.7	620	2	T19907	probable receptor
409	68.5	5.7	237	2	T25977	hypothetical prote	482	68	5.7	664	2	C84869	hypothetical prote
410	68.5	5.7	238	2	T04280	hypothetical prote	483	68	5.7	718	2	E83718	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote	484	68	5.7	804	2	T49975	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote	485	68	5.7	836	2	T18460	hypothetical prote
413	68.5	5.7	265	2	A13428	hypothetical prote	486	68	5.7	859	2	S69700	hypothetical prote
414	68.5	5.7	285	2	E86835	O-antigen export s	487	68	5.7	871	2	H72597	hypothetical prote
415	68.5	5.7	297	2	S74335	maltose ABC transp	488	68	5.7	1429	2	T19422	hypothetical prote
416	68.5	5.7	304	2	AG3035	carbon dioxide con	489	68	5.7	1878	2	E86189	hypothetical prote
417	68.5	5.7	304	2	D98250	hypothetical prote	490	68	5.7	3010	1	GNWVTC	genome polyprotein
418	68.5	5.7	343	2	AC2129	probable sugar ABC	491	67.5	5.6	104	2	T36801	conserved hypothet
419	68.5	5.7	359	2	B59105	iron(III) dictrat	492	67.5	5.6	200	2	H72295	hypothetical prote
420	68.5	5.7	362	2	D72424	hypothetical prote	493	67.5	5.6	273	2	A97700	hypothetical prote
421	68.5	5.7	377	1	JQ2337	oligopeptide ABC t	494	67.5	5.6	288	2	F72219	hypothetical prote
422	68.5	5.7	383	2	H53870	Edg-1 orphan recep	495	67.5	5.6	320	2	T23674	HHRF3 protein - hu
423	68.5	5.7	391	2	B81265	probable transmemb	496	67.5	5.6	323	1	QOBE3	NADH2 dehydrogenas
424	68.5	5.7	395	2	H83774	hypothetical prote	497	67.5	5.6	348	2	T12591	G protein-coupled
425	68.5	5.7	395	2	A96189	hypothetical prote	498	67.5	5.6	354	2	T09353	protein Tl1F1.1
426	68.5	5.7	395	2	AG3097	hypothetical prote	499	67.5	5.6	362	2	C88086	hypothetical prote
427	68.5	5.7	419	2	AG1660	conserved hypothet	500	67.5	5.6	387	2	T24581	mutants block spor
428	68.5	5.7	420	2	I51666	Mel-1c receptor su	501	67.5	5.6	397	2	AH3999	multidrug resistan
429	68.5	5.7	425	2	F97108	probable glycosylt	502	67.5	5.6	419	2	AH1288	sodium-dependent c
430	68.5	5.7	430	2	S15308	hypothetical prote	503	67.5	5.6	439	2	H83699	TDP-Fuc4NAC lipidi
431	68.5	5.7	431	2	H72247	preproteins translo	504	67.5	5.6	450	2	G91219	4-alpha-1-fucosylt
432	68.5	5.7	444	2	A48260	corticosterin rec	505	67.5	5.6	450	2	A86066	hypothetical prote
433	68.5	5.7	445	2	E22845	hypothetical prote	506	67.5	5.6	452	2	F65183	vasoactive intesti
434	68.5	5.7	479	2	T44326	hypothetical prote	507	67.5	5.6	459	2	JH0594	NADH2 dehydrogenas
435	68.5	5.7	480	2	B70446	hypothetical prote	508	67.5	5.6	483	2	G84113	sodium-dependent n
436	68.5	5.7	488	2	T15941	hypothetical prote	509	67.5	5.6	488	1	QXAS4	hypothetical prote
437	68.5	5.7	492	2	G90574	hypothetical prote	510	67.5	5.6	492	2	F64464	ADP, ATP carrier p
438	68.5	5.7	502	2	S77331	NADH2 dehydrogenas	511	67.5	5.6	498	2	T48262	choline transporte
439	68.5	5.7	512	2	T00605	probable cytochrom	512	67.5	5.6	516	2	H82973	gamma-aminobutyric
440	68.5	5.7	518	2	S50465	PAC2 protein - yea	513	67.5	5.6	516	2	A71259	probable dicarboxy
441	68.5	5.7	525	2	JN0902	pituitary adenylat	514	67.5	5.6	598	2	I51368	I8 protein - vacci
442	68.5	5.7	542	2	S58102	hypothetical prote	515	67.5	5.6	632	2	A71259	NPH-II, helicase -
443	68.5	5.7	558	2	F64235	Na+ ATPase chain J	516	67.5	5.6	676	1	W2V218	ATP/GTP-binding pr
444	68.5	5.7	634	2	C83530	potassium uptake p	517	67.5	5.6	676	2	T37345	hypothetical prote
445	68.5	5.7	670	2	G86702	potassium uptake p	518	67.5	5.6	676	2	D42511	L8R protein - vari
446	68.5	5.7	724	2	H86437	unknown protein [i	519	67.5	5.6	676	2	T28500	sensor histidine k
447	68.5	5.7	788	2	G64707	cation-transportin	520	67.5	5.6	682	2	D72158	hypothetical prote
448	68.5	5.7	923	1	MMBY7C	probable membrane	521	67.5	5.6	686	2	G82448	probable ATP-bindi
449	68.5	5.7	1004	1	S55353	probable copper-tr	522	67.5	5.6	716	1	T02567	vacuolar ATPase (E
450	68	5.7	146	2	H75201	hypothetical prote	523	67.5	5.6	740	2	T02567	hypothetical prote
451	68	5.7	205	2	A64373	hypothetical prote	524	67.5	5.6	838	2	A54163	hypothetical prote
452	68	5.7	255	2	F39925	hypothetical prote	525	67.5	5.6	866	2	T20574	hypothetical prote
453	68	5.7	266	2	C95316	probable ABC trans	526	67.5	5.6	950	2	T15915	hypothetical prote
454	68	5.7	270	2	AB3627	maltose transport	527	67.5	5.6	950	2	T15915	hypothetical prote
455	68	5.7	279	2	AG2165	bicarbonate transp	528	67.5	5.6	1159	2	T02866	hypothetical prote
456	68	5.7	294	2	T41953	G protein-coupled	529	67.5	5.6	1244	2	T19615	hypothetical prote
457	68	5.7	294	2	AE0004	ribonuclease BN (E	530	67.5	5.6	1411	2	S48442	hypothetical prote
458	68	5.7	313	2	B38888	COI intron 9 prote	531	67.5	5.6	1411	2	S48442	hypothetical prote
459	68	5.7	355	2	A45177	chemokine (C-C) re	532	67.5	5.6	1753	2	S30855	hypothetical prote
460	68	5.7	360	2	T11067	ubiquinol-cytochro	533	67.5	5.6	2332	1	GNMYF	hypothetical prote
461	68	5.7	364	2	JC2115	prostaglandin E re	534	67	5.6	151	2	A72093	genome polyprotein
462	68	5.7	365	2	JN0693	prostaglandin E2 r	535	67	5.6	151	2	H86529	conserved hypothet
463	68	5.7	370	2	H90559	hypothetical prote	536	67	5.6	159	2	S61040	probable membrane
464	68	5.7	379	2	S58450	ubiquinol-cytochro	537	67	5.6	180	2	I48129	Xel69 (escapes X-1
465	68	5.7	393	2	AG0184	probable multidrug	538	67	5.6	203	2	D70150	hypothetical prote
466	68	5.7	402	2	T41253	hypothetical wtf5	539	67	5.6	225	1	MMTHIB	E1 membrane glycop
467	68	5.7	417	2	T11387	NADH2 dehydrogenas	540	67	5.6	244	2	D70404	conserved hypothet

541 67 5.6 255 2 C90078 hypothetical prote
542 67 5.6 275 2 G98194 sugar ABC transpor
543 67 5.6 275 2 AC3092 hypothetical prote
544 67 5.6 275 2 S75698 hypothetical prote
545 67 5.6 276 2 F69307 conserved hypothet
546 67 5.6 276 2 S3527 DNA-damage repair
547 67 5.6 283 2 F96959 rRNA-processing ri
548 67 5.6 285 2 AE3024 hypothetical prote
549 67 5.6 286 2 D64235 hypothetical prote
550 67 5.6 314 2 D96703 hypothetical prote
551 67 5.6 317 2 D98260 inner membrane pro
552 67 5.6 336 2 A96997 ferrichrome transp
553 67 5.6 345 2 T21776 hypothetical prote
554 67 5.6 349 2 D84166 hypothetical prote
555 67 5.6 350 2 C88997 protein C50H11.2 l
556 67 5.6 352 2 T32314 hypothetical prote
557 67 5.6 379 2 S58451 ubiquinol-cytochro
558 67 5.6 379 2 S58449 ubiquinol-cytochro
559 67 5.6 396 1 C69291 pheromone shutdown
560 67 5.6 407 2 E70309 hypothetical prote
561 67 5.6 411 2 B71500 probable amino aci
562 67 5.6 415 2 S74041 pyruvate synthase
563 67 5.6 416 2 T46401 hypothetical prote
564 67 5.6 423 2 C95085 sodium-dependent t
565 67 5.6 436 2 AC1021 proton glutamate s
566 67 5.6 441 2 F86279 hypothetical prote
567 67 5.6 446 2 G72287 hypothetical prote
568 67 5.6 496 2 A31986 glucose transpote
569 67 5.6 507 2 AB1707 glycine betaine tr
570 67 5.6 516 2 AE0655 probable membrane
571 67 5.6 616 2 JC7777 ATP binding cassel
572 67 5.6 717 2 T49238 hypothetical prote
573 67 5.6 753 2 S58331 dolichyl-phosphate
574 67 5.6 769 2 F81415 DNA topoisomerase
575 67 5.6 784 2 C82679 cell division prot
576 67 5.6 787 2 FN0677 hypothetical prote
577 67 5.6 798 2 T34248 hypothetical prote
578 67 5.6 814 2 T05537 probable serine/th
579 67 5.6 823 2 T35230 probable integral
580 67 5.6 880 2 D69427 conserved hypothet
581 67 5.6 891 2 B82495 probable NADH dehy
582 67 5.6 900 2 E69631 galactosamine-cont
583 67 5.6 1175 2 S39951 chitin synthase (E
584 67 5.6 1242 1 DJBEC1 DNA-directed DNA p
585 67 5.6 1333 2 S63403 probable membrane
586 67 5.6 1511 2 A53151 pleiotropic drug r
587 67 5.6 1575 2 G82905 conserved hypothet
588 67 5.6 1879 2 T19481 hypothetical prote
589 67 5.6 1905 2 T18267 multidrug resistan
590 67 5.6 1993 2 T30902 sodium channel SCA
591 67 5.6 3010 1 GNVWCJ genome polypeptide
592 66.5 5.6 153 1 G69847 conserved hypothet
593 66.5 5.6 203 2 T28732 hypothetical prote
594 66.5 5.6 204 2 C70506 hypothetical prote
595 66.5 5.6 218 2 C64586 cag pathogenicity
596 66.5 5.6 245 2 A81405 sec-independent pr
597 66.5 5.6 263 2 A12384 hypothetical prote
598 66.5 5.6 268 2 A70417 hypothetical prote
599 66.5 5.6 272 2 AI0075 probable permease
600 66.5 5.6 279 1 S56664 nitrate transport
601 66.5 5.6 279 2 E70322 hypothetical prote
602 66.5 5.6 293 2 A84110 sugar ABC transpor
603 66.5 5.6 294 2 S70876 hypothetical prote
604 66.5 5.6 316 2 F81712 ABC transporter, p
605 66.5 5.6 333 2 S77103 hypothetical prote
606 66.5 5.6 347 2 AD2201 hypothetical prote
607 66.5 5.6 356 2 T20737 hypothetical prote
608 66.5 5.6 359 2 F90055 conserved hypothet
609 66.5 5.6 367 2 S75836 hypothetical prote
610 66.5 5.6 380 2 G89786 hypothetical prote
611 66.5 5.6 384 1 I38890 dual specificity p
612 66.5 5.6 389 2 E96516 F16N3.13 [imported
613 66.5 5.6 400 2 G00013 D3 dopamine recept

614 66.5 5.6 614 2 G89773
615 66.5 5.6 412 2 H95041
616 66.5 5.6 413 2 D98111
617 66.5 5.6 435 2 G95246
618 66.5 5.6 435 2 B95135
619 66.5 5.6 462 2 H71228
620 66.5 5.6 488 2 G71969
621 66.5 5.6 490 2 D84998
622 66.5 5.6 490 2 AC6391
623 66.5 5.6 491 2 AC1555
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625 66.5 5.6 494 2 T32644
626 66.5 5.6 507 2 T27627
627 66.5 5.6 539 2 G83720
628 66.5 5.6 547 2 E91135
629 66.5 5.6 563 2 H85980
630 66.5 5.6 550 1 A48026
631 66.5 5.6 582 2 C71424
632 66.5 5.6 583 2 AI1510
633 66.5 5.6 598 2 T32430
634 66.5 5.6 663 2 AG2696
635 66.5 5.6 663 2 G97478
636 66.5 5.6 727 2 I56506
637 66.5 5.6 727 2 S27043
638 66.5 5.6 782 2 S19876
639 66.5 5.6 862 2 B36786
640 66.5 5.6 889 2 T47311
641 66.5 5.6 992 2 T27479
642 66.5 5.6 1014 2 T31433
643 66.5 5.6 1083 2 C88854
644 66.5 5.6 1144 2 H81037
645 66.5 5.6 1456 2 T15961
646 66.5 5.6 1684 2 JW0057
647 66.5 5.6 1768 2 B85062
648 66.5 5.6 2151 1 S16449
649 66.5 5.6 2285 1 G02434
650 66.5 5.6 2833 2 AC3360
651 66.5 5.6 3011 1 GNVWC3
652 66 5.5 93 2 S28759
653 66 5.5 130 2 D83820
654 66 5.5 209 2 A89801
655 66 5.5 276 2 H96816
656 66 5.5 279 2 S42125
657 66 5.5 285 2 D87447
658 66 5.5 302 2 A99074
659 66 5.5 305 2 I47040
660 66 5.5 317 1 B41671
661 66 5.5 318 2 B84291
662 66 5.5 322 2 E71137
663 66 5.5 332 2 C97272
664 66 5.5 370 1 I52315
665 66 5.5 379 1 S17405
666 66 5.5 379 1 S17405
667 66 5.5 379 2 S58460
668 66 5.5 381 2 A35300
669 66 5.5 390 1 QQBET9
670 66 5.5 397 2 T21154
671 66 5.5 397 2 T44477
672 66 5.5 397 2 B70505
673 66 5.5 401 2 T44831
674 66 5.5 404 1 B64927
675 66 5.5 404 2 A85777
676 66 5.5 404 2 B90928
677 66 5.5 411 2 H86539
678 66 5.5 412 2 A82444
679 66 5.5 418 2 T41027
680 66 5.5 418 2 B72353
681 66 5.5 424 2 T07366
682 66 5.5 436 2 T14816
683 66 5.5 447 2 T18633
684 66 5.5 450 2 A37223
685 66 5.5 450 2 A38316
686 66 5.5 453 2 F86846

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alpha-2-adrenergic
ABC transporter pe

687	66	5.5	483	2	S75369	hypotheical prote	760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
688	66	5.5	484	2	T24238	hypotheical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	496	2	E82940	hypotheical prote	762	65.5	5.5	578	2	T15736	hypotheical prote
690	66	5.5	508	2	G47677	hypotheical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	2	T28306	ORF MSV145 hypothe	764	65.5	5.5	590	2	C81316	probable sugar epi
692	66	5.5	527	2	G69635	PTS arbutin-like e	765	65.5	5.5	597	2	B82881	hypotheical prote
693	66	5.5	532	2	A90037	hypotheical prote	766	65.5	5.5	617	2	AB1167	phosphotransferase
694	66	5.5	546	2	A69890	hypotheical prote	767	65.5	5.5	618	2	AB1204	phosphotransferase
695	66	5.5	548	2	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	H70331	ATP-dependent heli
696	66	5.5	552	2	S45886	hypotheical prote	769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
697	66	5.5	555	2	S73707	Na(+)-translocatin	770	65.5	5.5	720	2	H82198	RTX toxin transpor
698	66	5.5	570	2	S07744	NADH2 dehydrogenas	771	65.5	5.5	721	2	AF1254	penicillin-binding
699	66	5.5	573	1	S33212	INDAI protein - fu	772	65.5	5.5	740	2	S61568	probable membrane
700	66	5.5	573	2	AF1418	ABC transporter, A	773	65.5	5.5	860	1	QRHULD	LDL receptor precu
701	66	5.5	573	2	AH1793	ABC transporter, A	774	65.5	5.5	958	2	AC0204	probable integral
702	66	5.5	619	2	T11314	NADH2 dehydrogenas	775	65.5	5.5	1087	1	S41797	cellulose 1,4-beta
703	66	5.5	632	2	T24405	hypotheical prote	776	65.5	5.5	1328	2	B22999	TYB protein - yea
704	66	5.5	654	2	A98350	hypotheical ABC t	777	65.5	5.5	1427	2	S74293	SRB8 protein - yea
705	66	5.5	705	2	AF2932	hypotheical prote	778	65.5	5.5	1581	2	B71636	hypotheical prote
706	66	5.5	721	2	T48464	hypotheical prote	779	65.5	5.5	1635	2	T34452	hypotheical prote
707	66	5.5	721	2	A70764	probable glgX prot	780	65	5.4	126	2	AD0340	probable membrane
708	66	5.5	736	2	G01522	acidic 82 kDa prot	781	65	5.4	149	2	C69393	transcription regu
709	66	5.5	784	2	B90442	tricorn proteinase	782	65	5.4	176	1	Q1AD25	early E1B 21K prot
710	66	5.5	1039	2	S76747	hypotheical prote	783	65	5.4	196	2	S40728	hypotheical prote
711	66	5.5	1054	2	A61221	probable calcium t	784	65	5.4	225	1	MMTHIV	E1 membrane glycop
712	66	5.5	1359	2	T34036	hypotheical prote	785	65	5.4	247	2	I48149	serotonin receptor
713	66	5.5	1375	2	S48375	hypotheical prote	786	65	5.4	257	2	B75099	hypotheical prote
714	66	5.5	2599	2	F90608	ABC transporter pe	787	65	5.4	259	2	A47112	growth response pr
715	66	5.5	26926	1	I38344	titin, cardiac mus	788	65	5.4	271	2	E89950	hema concentration
716	65.5	5.5	132	2	E97760	NADH2 dehydrogenas	789	65	5.4	280	2	S75957	nitrate transport
717	65.5	5.5	132	2	E70074	hypotheical prote	790	65	5.4	290	2	T02877	probable chlorophy
718	65.5	5.5	146	2	G69447	hypotheical prote	791	65	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	2	AI3476	signal peptidase I	792	65	5.4	291	2	A32671	cytochrome c oxida
720	65.5	5.5	197	2	T17106	hypotheical prote	793	65	5.4	307	2	B36125	branched-chain ami
721	65.5	5.5	210	2	S67771	endoplasmic reticu	794	65	5.4	313	2	A64084	lysophospholipase
722	65.5	5.5	252	2	T43100	hypotheical prote	795	65	5.4	319	2	D87087	hypotheical prote
723	65.5	5.5	280	2	F69456	signal sequence pe	796	65	5.4	322	2	S38091	hypotheical prote
724	65.5	5.5	297	2	F68639	phosphate ABC tran	797	65	5.4	330	2	H75068	dipeptide abc tran
725	65.5	5.5	297	2	E83792	hypotheical prote	798	65	5.4	335	2	H75029	hypotheical prote
726	65.5	5.5	301	2	T21308	hypotheical prote	799	65	5.4	338	2	S50339	NADH2 dehydrogenas
727	65.5	5.5	317	2	S23459	polysulfide reduct	800	65	5.4	344	2	AD1200	conserved hypothe
728	65.5	5.5	327	2	T36087	probable binding p	801	65	5.4	345	2	T12361	NADH2 dehydrogenas
729	65.5	5.5	348	1	S36003	NADH2 dehydrogenas	802	65	5.4	355	2	G70200	hypotheical prote
730	65.5	5.5	351	2	F82880	hypotheical ferrit	803	65	5.4	359	2	T15249	hypotheical prote
731	65.5	5.5	365	1	F69629	spore germination	804	65	5.4	362	2	H69785	mannan endo-1,4-be
732	65.5	5.5	367	2	JC2056	prostaglandin B2 r	805	65	5.4	375	2	I38879	corticotropin rele
733	65.5	5.5	379	2	S58456	ubiquinol-cytochro	806	65	5.4	379	1	S17414	ubiquinol-cytochro
734	65.5	5.5	379	2	T32778	hypotheical prote	807	65	5.4	379	2	S58461	ubiquinol-cytochro
735	65.5	5.5	391	2	T32601	hypotheical prote	808	65	5.4	379	2	S58455	ubiquinol-cytochro
736	65.5	5.5	394	2	AH0362	nucleoside permeas	809	65	5.4	380	1	D34285	ubiquinol-cytochro
737	65.5	5.5	410	2	T11064	NADH2 dehydrogenas	810	65	5.4	382	2	T11138	ubiquinol-cytochro
738	65.5	5.5	423	2	E90569	conserved hypothe	811	65	5.4	390	2	C84984	hypotheical prote
739	65.5	5.5	425	2	A97688	hypotheical 45.5K	812	65	5.4	415	2	T21532	hypotheical prote
740	65.5	5.5	425	2	AF2913	conserved hypothe	813	65	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	2	T32832	hypotheical prote	814	65	5.4	442	2	A83122	probable MFS trans
742	65.5	5.5	442	2	A42670	microfibril-associ	815	65	5.4	445	2	AD2358	glucosyltransferas
743	65.5	5.5	445	2	T38916	probable transcrip	816	65	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	2	H83629	probable dicarboxy	817	65	5.4	462	2	B88613	protein T27B9.5 [1
745	65.5	5.5	457	2	A75327	hypotheical prote	818	65	5.4	477	2	S45508	probable membrane
746	65.5	5.5	477	2	B75170	hypotheical prote	819	65	5.4	479	2	A69036	TRK system potassi
747	65.5	5.5	480	2	A60043	endoplasmic reticu	820	65	5.4	481	2	E81050	cytochrome-c oxida
748	65.5	5.5	487	2	A97928	type I site-specif	821	65	5.4	490	2	T14545	probable sugar tra
749	65.5	5.5	488	1	H64537	cytochrome-c oxida	822	65	5.4	492	2	T59107	NADH2 dehydrogenas
750	65.5	5.5	488	2	G81295	cytochrome-c oxida	823	65	5.4	510	2	S55204	hypotheical prote
751	65.5	5.5	491	2	A81197	efflux transporter	824	65	5.4	511	2	H75097	polyaccharide bio
752	65.5	5.5	495	2	A97022	probably membrane	825	65	5.4	513	2	T37180	probable membrane
753	65.5	5.5	500	2	G84706	hypotheical prote	826	65	5.4	526	2	D91047	hydrogenase 4 memb
754	65.5	5.5	502	2	AD3395	NADH2 dehydrogenas	827	65	5.4	530	2	B89771	hypotheical prote
755	65.5	5.5	502	2	T25669	hypotheical prote	828	65	5.4	535	2	A64697	conserved hypothe
756	65.5	5.5	518	2	A53207	probable folate tr	829	65	5.4	539	2	S55190	hypotheical prote
757	65.5	5.5	528	2	T34417	delayed rectifier	830	65	5.4	547	2	T31543	hypotheical prote
758	65.5	5.5	544	2	B84825	probable ABC trans	831	65	5.4	547	2	S53920	SNG1 protein - yea
759	65.5	5.5	545	2	B90460	hypotheical prote	832	65	5.4	576	2	T25375	hypotheical prote

833	65	5.4	579	2	S61131	probable membrane	906	64.5	5.4	495	2	S39061	pituitary adenyllyl
834	65	5.4	608	2	S65298	dicarboxylic amino	907	64.5	5.4	495	2	S36114	pituitary adenylat
835	65	5.4	611	2	T21747	hypothetical prote	908	64.5	5.4	512	2	H64964	probable membrane
836	65	5.4	624	2	G82508	hypothetical prote	909	64.5	5.4	521	2	A99549	amino acid permeas
837	65	5.4	627	2	T11125	NADH2 dehydrogenas	910	64.5	5.4	523	2	S39060	pituitary adenyllyl
838	65	5.4	633	2	F84483	Mutator-like trans	911	64.5	5.4	547	2	H65107	hypothetical 61.6
839	65	5.4	638	2	D69957	conserved hypothet	912	64.5	5.4	554	2	A56730	carl protein - Pod
840	65	5.4	643	2	F97787	sodium/pantothenat	913	64.5	5.4	555	2	B97812	virulence factor m
841	65	5.4	676	2	A45515	dnak-type molecula	914	64.5	5.4	575	2	AB1793	ABC transporter (A
842	65	5.4	684	2	F86394	protein T24P13.20	915	64.5	5.4	576	2	T05904	cytochrome P450 97
843	65	5.4	697	2	H84791	hypothetical prote	916	64.5	5.4	614	2	B89869	hypothetical prote
844	65	5.4	702	2	T13505	NADH2 dehydrogenas	917	64.5	5.4	622	2	AC1236	acyltransferase (t
845	65	5.4	705	2	T04400	NADH2 dehydrogenas	918	64.5	5.4	638	1	Q0BY2M	mRNA maturase b14
846	65	5.4	713	2	H96818	hypothetical prote	919	64.5	5.4	715	2	T26307	hypothetical prote
847	65	5.4	773	2	G83816	late competence op	920	64.5	5.4	720	2	T47648	ABC transporter-11
848	65	5.4	808	2	T04459	hypothetical prote	921	64.5	5.4	721	2	AD1617	penicillin-binding
849	65	5.4	861	2	S77086	hypothetical prote	922	64.5	5.4	721	2	AE1491	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN	923	64.5	5.4	735	2	AD0341	probable membrane
851	65	5.4	931	2	F84637	probable plasma me	924	64.5	5.4	763	2	AD1070	phosphatidylglycer
852	65	5.4	938	2	T01809	hypothetical prote	925	64.5	5.4	801	2	A89862	Na+/H+ antiporter
853	65	5.4	1089	2	C70522	probable mmp18 pro	926	64.5	5.4	803	2	H64568	histidine kinase -
854	65	5.4	1163	2	D64315	type I restriction	927	64.5	5.4	889	2	T30715	probable major cor
855	65	5.4	1178	2	S76370	sensory transducti	928	64.5	5.4	979	2	JC0848	probable membrane
856	65	5.4	1232	2	I38496	anion exchanger 3	929	64.5	5.4	1007	2	JC0866	138K protein - Tet
857	65	5.4	1421	2	T34325	hypothetical prote	930	64.5	5.4	1114	2	JH0284	125K surface antig
858	65	5.4	5069	2	T17464	rifamycin polyketi	931	64.5	5.4	1146	2	B70723	probable mmp112 pr
859	64.5	5.4	180	2	T41339	hypothetical prote	932	64.5	5.4	1154	2	T48829	related to SREBP c
860	64.5	5.4	211	2	S35280	eac protein - phag	933	64.5	5.4	1465	2	S45628	DNA-directed DNA p
861	64.5	5.4	217	2	AE0395	probable amino aci	934	64.5	5.4	1529	2	S69688	hypothetical prote
862	64.5	5.4	227	2	C69432	hypothetical prote	935	64.5	5.4	1630	2	S64403	ESPI protein - yea
863	64.5	5.4	234	2	E96957	HAD superfamily hy	936	64.5	5.4	1651	2	S64800	probable membrane
864	64.5	5.4	268	2	AF2470	potassium channel	937	64.5	5.4	3033	1	GNWVJ8	genome polyprotein
865	64.5	5.4	271	2	B81384	prolipoprotein dia	938	64	5.4	202	2	A70041	conserved hypothet
866	64.5	5.4	275	2	T43119	hypothetical prote	939	64	5.4	209	2	G82359	conserved hypothet
867	64.5	5.4	293	2	D71517	probable metal tra	940	64	5.4	253	2	JC5347	cd33 protein - Clo
868	64.5	5.4	295	2	T23202	hypothetical prote	941	64	5.4	259	2	T12451	hypothetical prote
869	64.5	5.4	297	2	T27584	hypothetical prote	942	64	5.4	259	2	H69768	conserved hypothet
870	64.5	5.4	320	2	T23904	hypothetical prote	943	64	5.4	270	2	F89632	protein F1386.3 [i
871	64.5	5.4	326	2	A86411	protein F3M18.6 [i	944	64	5.4	274	2	T50567	probable ABC-type
872	64.5	5.4	353	2	F64175	hypothetical prote	945	64	5.4	276	2	C70040	plant-metabolite d
873	64.5	5.4	358	2	T22823	hypothetical prote	946	64	5.4	276	2	S48358	probable membrane
874	64.5	5.4	361	2	A86841	hypothetical prote	947	64	5.4	281	2	C95932	probable sugar upt
875	64.5	5.4	361	2	A40734	Pas (Passover) pro	948	64	5.4	283	2	D83009	probable permease
876	64.5	5.4	379	1	S43264	ubiquinol-cytochro	949	64	5.4	285	2	B83883	sugar transport sy
877	64.5	5.4	379	2	T11505	ubiquinol-cytochro	950	64	5.4	288	2	S36955	cytochrome-c oxida
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro	951	64	5.4	330	2	T29675	hypothetical prote
879	64.5	5.4	379	2	A53077	ubiquinol-cytochro	952	64	5.4	342	2	A48258	dopamine receptor
880	64.5	5.4	381	1	C8MS	ubiquinol-cytochro	953	64	5.4	347	2	T11248	NADH2 dehydrogenas
881	64.5	5.4	381	2	S33449	pituitary adenylat	954	64	5.4	351	2	S56716	protein kinase SPK
882	64.5	5.4	385	2	H69154	hypothetical prote	955	64	5.4	351	2	G01430	Plu protein - huma
883	64.5	5.4	398	2	H95057	phosphoglycerate k	956	64	5.4	367	2	T20271	hypothetical prote
884	64.5	5.4	398	2	A97927	phosphoglycerate k	957	64	5.4	369	2	H90587	hypothetical prote
885	64.5	5.4	400	2	G01977	d3 dopamine recept	958	64	5.4	370	1	S26031	ubiquinol-cytochro
886	64.5	5.4	411	2	S46800	LAG1 protein - yea	959	64	5.4	376	2	G82656	twitching motility
887	64.5	5.4	416	2	AF1127	rod shape-determin	960	64	5.4	378	2	D64181	probable cytochrom
888	64.5	5.4	426	2	T45800	UDP-N-acetylglucos	961	64	5.4	379	1	CBBO	ubiquinol-cytochro
889	64.5	5.4	433	2	T11162	NADH2 dehydrogenas	962	64	5.4	379	1	S17419	ubiquinol-cytochro
890	64.5	5.4	435	2	AC0105	probable maltodext	963	64	5.4	379	1	S26163	ubiquinol-cytochro
891	64.5	5.4	439	2	C22845	NADH2 dehydrogenas	964	64	5.4	379	1	S43263	ubiquinol-cytochro
892	64.5	5.4	439	2	A84153	hypothetical prote	965	64	5.4	379	2	T11414	ubiquinol-cytochro
893	64.5	5.4	443	2	B26696	hypothetical prote	966	64	5.4	379	2	S58452	ubiquinol-cytochro
894	64.5	5.4	444	2	T11474	NADH2 dehydrogenas	967	64	5.4	379	2	S58459	ubiquinol-cytochro
895	64.5	5.4	444	2	A43676	P44 hepatitis-asso	968	64	5.4	383	2	S55594	G protein-coupled
896	64.5	5.4	444	2	S48218	microtubular aggre	969	64	5.4	383	2	G74667	NA+/H+ antiporter
897	64.5	5.4	446	1	DYRTD3	dopamine receptor	970	64	5.4	383	2	H1848	probable na+/h+ an
898	64.5	5.4	448	2	D85362	hypothetical prote	971	64	5.4	387	2	S74522	hypothetical prote
899	64.5	5.4	448	2	S57909	probable histidine	972	64	5.4	402	2	AD1417	drug-efflux transp
900	64.5	5.4	450	2	T23528	hypothetical prote	973	64	5.4	404	2	A97559	hypothetical prote
901	64.5	5.4	451	2	D70045	two-component sens	974	64	5.4	404	2	AE2779	acyltransferase [i
902	64.5	5.4	467	2	JN0616	pituitary adenylat	975	64	5.4	409	2	S26021	NADH2 dehydrogenas
903	64.5	5.4	478	2	C29051	transposase C - Ba	976	64	5.4	411	2	A55610	corticotropin-rele
904	64.5	5.4	478	2	FWSV22	glycinin chain Ala	977	64	5.4	413	2	H81659	branched-chain ami
905	64.5	5.4	495	2	S10851	glycinin G1 precur	978	64	5.4	422	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malC protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	B40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
981	64	5.4	451	2	A36308	spore cortex penic	1054	63.5	5.3	328	2	T39824	septin homolog - f
982	64	5.4	455	2	T31258	aromatic oxygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
983	64	5.4	457	2	AF2975	aminotransferase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	spA40 protein - Sh
986	64	5.4	469	2	H03222	polysaccharide bio	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	E58931	NADH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	503	2	JC7627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	oligopeptide prote
990	64	5.4	527	2	A75122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	hypothetical prote
991	64	5.4	536	2	T36109	hypothetical prote	1064	63.5	5.3	372	2	S26667	oligopeptide trans
992	64	5.4	538	2	C90406	conserved hypotnet	1065	63.5	5.3	377	2	B72275	G protein-coupled
993	64	5.4	544	2	T13877	NADH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	Probable aspartate
994	64	5.4	562	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
995	64	5.4	575	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K10B4.2 (i
996	64	5.4	586	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	598	2	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable hth trans
998	64	5.4	602	2	C75120	hypothetical prote	1071	63.5	5.3	395	2	H81358	transmembrane tran
999	64	5.4	606	2	B69805	conserved hypotnet	1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1000	64	5.4	608	2	G02640	polycystic kidney	1073	63.5	5.3	399	2	B95080	probable periplasm
1001	64	5.4	609	2	F70512	probable ATPase -	1074	63.5	5.3	400	2	AG3016	cell division prot
1002	64	5.4	610	2	S37049	H+-exporting ATPas	1075	63.5	5.3	401	2	T46306	phosphoglycerate k
1003	64	5.4	614	2	A69845	Na+/H+ antiporter	1076	63.5	5.3	404	1	LABECA	hypothetical prote
1004	64	5.4	614	2	T47177	hypothetical prote	1077	63.5	5.3	406	2	T19887	latent membrane pr
1005	64	5.4	654	2	C86677	DNA ligase (NAD) (1078	63.5	5.3	423	2	T04915	hypothetical prote
1006	64	5.4	657	2	T52460	hypothetical prote	1079	63.5	5.3	423	2	G85255	CDD-diacylglycerol
1007	64	5.4	661	2	T51779	non-phototropic hy	1080	63.5	5.3	426	2	A96268	phosphoglycerate k
1008	64	5.4	674	2	T50347	hypothetical prote	1081	63.5	5.3	426	2	T33299	hypothetical prote
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	438	2	A82262	conserved hypotnet
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	444	2	B85789	hypothetical prote
1011	64	5.4	802	2	A87754	protein C43E11.11	1084	63.5	5.3	445	2	T16025	hypothetical prote
1012	64	5.4	838	2	H82939	conserved hypotnet	1085	63.5	5.3	447	2	F90940	CDD-diacylglycerol
1013	64	5.4	860	2	T37768	probable vacuolar	1086	63.5	5.3	447	2	S52437	hypothetical prote
1014	64	5.4	874	2	B86322	FeAl4.8 protein -	1087	63.5	5.3	450	2	E96738	hypothetical prote
1015	64	5.4	896	2	AF1409	the two components	1088	63.5	5.3	452	2	C97187	sugar transferase
1016	64	5.4	991	2	S57385	probable membrane	1089	63.5	5.3	461	2	T27118	mg2+ transport pro
1017	64	5.4	1024	1	RN2QBP	DNA-directed RNA p	1090	63.5	5.3	468	2	T48686	hypothetical prote
1018	64	5.4	1078	2	T19745	hypothetical prote	1091	63.5	5.3	485	2	H90562	hypothetical prote
1019	64	5.4	1081	2	B81303	probable membrane	1092	63.5	5.3	487	2	B95059	hypothetical prote
1020	64	5.4	1227	2	A33638	erythrocyte anion	1093	63.5	5.3	491	2	A64939	sugar transport re
1021	64	5.4	1385	2	T13415	hypothetical prote	1094	63.5	5.3	492	2	B90373	integral membrane
1022	64	5.4	1462	1	DJHUAC	DNA-directed DNA p	1095	63.5	5.3	494	2	T76516	transporter like p
1023	64	5.4	1695	2	JB0084	voltage-gated sodi	1096	63.5	5.3	498	2	T48385	hypothetical prote
1024	64	5.4	2495	2	A71616	secreted protein p	1097	63.5	5.3	498	2	AF2325	hypothetical prote
1025	63.5	5.3	111	2	S43115	acidic ribosomal p	1098	63.5	5.3	500	2	G90321	virulence factor m
1026	63.5	5.3	123	2	G71692	NADH2 dehydrogenas	1099	63.5	5.3	511	2	A70201	nucleocapsid prote
1027	63.5	5.3	147	2	AH0495	probable membrane	1100	63.5	5.3	512	2	A49601	conserved hypotnet
1028	63.5	5.3	149	2	H70581	hypothetical prote	1101	63.5	5.3	525	2	G82873	sterol O-acyltans
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	537	2	I49454	uncharacterized me
1030	63.5	5.3	214	2	C90191	conserved hypotnet	1103	63.5	5.3	540	1	I49454	1-lactate permease
1031	63.5	5.3	218	2	B71925	cag island protein	1104	63.5	5.3	544	2	C96943	1-lactate permease
1032	63.5	5.3	218	2	T29205	hypothetical prote	1105	63.5	5.3	551	2	E64537	probable peptidase
1033	63.5	5.3	231	2	F85679	probable antiopre	1106	63.5	5.3	551	2	D71969	probable L-lactate
1034	63.5	5.3	238	2	S75336	hypothetical prote	1107	63.5	5.3	551	2	C96744	probable L-lactate
1035	63.5	5.3	241	2	F86691	ABC transporter pe	1108	63.5	5.3	567	2	T17588	hyaluronoglucosami
1036	63.5	5.3	242	1	S74794	hypothetical prote	1109	63.5	5.3	568	2	I46528	sodium/dicarboxyla
1037	63.5	5.3	246	2	AD3574	branched-chain ami	1110	63.5	5.3	593	2	E88956	protein ZK697.5 [i
1038	63.5	5.3	259	2	AF0106	probable membrane	1111	63.5	5.3	594	2	A36361	glucose transport
1039	63.5	5.3	275	2	E95161	hypothetical prote	1112	63.5	5.3	605	2	A36361	probable flagellar
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	H71562	hypothetical prote
1041	63.5	5.3	276	2	G84320	conserved membrane	1114	63.5	5.3	605	2	T43974	hypothetical prote
1042	63.5	5.3	276	2	E96951	hypothetical prote	1115	63.5	5.3	610	2	T44161	ba-type ubiquinol
1043	63.5	5.3	280	2	T16240	probable ABC trans	1116	63.5	5.3	668	2	B54759	protein kinase C (
1044	63.5	5.3	282	2	A80346	conserved hypotnet	1117	63.5	5.3	671	2	B37237	probable type III
1045	63.5	5.3	282	2	E83086	hypothetical prote	1118	63.5	5.3	681	2	AF0697	hypothetical prote
1046	63.5	5.3	291	2	E82939	hypothetical prote	1119	63.5	5.3	681	2	A85044	killer toxin KHS p
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	JQ1148	hypothetical prote
1048	63.5	5.3	291	2	F75571	NADH2 dehydrogenas	1121	63.5	5.3	708	2	T20314	probable transport
1049	63.5	5.3	313	2	D26696	hypothetical prote	1122	63.5	5.3	741	2	T48189	cell division prot
1050	63.5	5.3	315	2	E69365	ferrichrome ABC tr	1123	63.5	5.3	780	2	T48189	
1051	63.5	5.3	316	2	H86665		1124	63.5	5.3	787	2	A70132	

1125	63.5	5.3	819	2	T19351	hypothetical prote	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical prote	1199	63	5.3	481	2	S60260	stomatin-like prot
1127	63.5	5.3	843	2	T32487	hypothetical prote	1200	63	5.3	490	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	conserved hypothet	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	844	2	AD2339	hypothetical prote	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08987	probable cadmium-t	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97917	hypothetical prote	1204	63	5.3	508	2	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87323	hypothetical prote	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1098	2	S38100	hypothetical prote	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1229	2	S42391	hypothetical prote	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1351	2	C71607	hypothetical prote	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1388	2	T17269	hypothetical prote	1209	63	5.3	534	2	A99316	hypothetical prote
1137	63.5	5.3	1407	1	T00558	probable ABC trans	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1408	2	T47671	P-glycoprotein-lik	1211	63	5.3	582	2	B70081	hypothetical prote
1139	63.5	5.3	1545	2	T42751	sulfonylurea recep	1212	63	5.3	565	2	B86359	protein similar to
1140	63.5	5.3	1545	2	T46645	sulfonylurea recep	1213	63	5.3	569	2	C70136	flagellar basal-bo
1141	63.5	5.3	1769	2	S53378	probable membrane	1214	63	5.3	574	2	T47566	hypothetical prote
1142	63.5	5.3	2357	2	A59249	Class VII unconven	1215	63	5.3	579	2	AB2177	hypothetical prote
1143	63.5	5.3	4725	1	A44357	dynein heavy chain	1216	63	5.3	583	2	G84829	probable PT2 fami
1144	63	5.3	96	1	WNV253	F3 protein - fowlp	1217	63	5.3	584	2	G89789	two-component sens
1145	63	5.3	103	2	T20878	hypothetical prote	1218	63	5.3	598	2	S66954	probable membrane
1146	63	5.3	175	2	D70945	hypothetical prote	1219	63	5.3	600	2	B83875	two-component sens
1147	63	5.3	230	2	B81705	conserved hypothet	1220	63	5.3	608	2	AD2000	ABC transporter AT
1148	63	5.3	230	2	T17506	hypothetical prote	1221	63	5.3	677	2	T26574	hypothetical prote
1149	63	5.3	236	2	F83520	phosphoribosylamin	1222	63	5.3	677	2	P95310	probable membrane-
1150	63	5.3	249	2	T01891	hypothetical prote	1223	63	5.3	682	1	H64485	replication licens
1151	63	5.3	257	2	S01165	achaeate-scute locu	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1152	63	5.3	258	2	H65188	sec-independent pr	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1153	63	5.3	258	2	F86071	sec-independent pr	1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1154	63	5.3	258	2	H91224	Sec-independent pr	1227	63	5.3	712	2	D87418	proton pump, proba
1155	63	5.3	280	2	D84015	maltose/maltodextr	1228	63	5.3	729	2	T06127	probable sugar tra
1156	63	5.3	288	2	S36954	cytochrome-C oxida	1229	63	5.3	737	2	I39547	S-protein secretio
1157	63	5.3	301	2	S48301	geranylgeranyl tra	1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	hypothetical prote	1231	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	306	2	H83620	probable permease	1232	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	A86743	hypothetical prote	1233	63	5.3	849	2	C87740	protein H26B21.2 [
1161	63	5.3	322	2	E90013	hypothetical prote	1234	63	5.3	869	2	S49844	probable membrane
1162	63	5.3	329	2	B87790	protein B0207.4 [i	1235	63	5.3	943	2	B45082	neurotrophic recep
1163	63	5.3	332	2	B84943	hypothetical prote	1236	63	5.3	960	2	T17297	hypothetical prote
1164	63	5.3	339	2	D89880	conserved hypothet	1237	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	NADH2 dehydrogenas	1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1166	63	5.3	358	2	B83808	hypothetical prote	1239	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	probable serine/th	1240	63	5.3	1212	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	prostaglandin E re	1241	63	5.3	1227	2	B34911	band 3-related pro
1169	63	5.3	362	2	T29552	hypothetical prote	1242	63	5.3	1532	2	T18438	hypothetical prote
1170	63	5.3	362	2	C69804	surface adhesion h	1243	63	5.3	1646	2	JH0422	voltage-dependent
1171	63	5.3	364	2	S65009	prostaglandin E re	1244	63	5.3	1854	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	prostaglandin E re	1245	63	5.3	2203	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17412	ubiquinol-cytochro	1246	63	5.3	2295	2	B71621	probable membrane
1174	63	5.3	379	1	S17413	ubiquinol-cytochro	1247	63	5.3	4488	1	RR1HM2	genome polyprotein
1175	63	5.3	379	1	S41833	ubiquinol-cytochro	1248	62.5	5.2	107	2	B69262	hypothetical prote
1176	63	5.3	379	1	S41847	ubiquinol-cytochro	1249	62.5	5.2	140	2	B86739	potassium channel
1177	63	5.3	379	1	S43265	ubiquinol-cytochro	1250	62.5	5.2	149	2	B83851	hypothetical prote
1178	63	5.3	379	2	T11492	ubiquinol-cytochro	1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1179	63	5.3	379	2	S58085	ubiquinol-cytochro	1252	62.5	5.2	173	2	D71702	hypothetical prote
1180	63	5.3	379	2	S58464	ubiquinol-cytochro	1253	62.5	5.2	178	2	S67379	hypothetical prote
1181	63	5.3	382	2	S47882	ubiquinol-cytochro	1254	62.5	5.2	181	2	G82911	hypothetical prote
1182	63	5.3	386	2	S60646	NADH2 dehydrogenas	1255	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	aromatic amino aci	1256	62.5	5.2	222	2	T22898	hypothetical prote
1184	63	5.3	389	2	C97876	aspartate transami	1257	62.5	5.2	236	2	F83705	hypothetical prote
1185	63	5.3	391	2	D64541	molybdopterin bios	1258	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	cell division prot	1259	62.5	5.2	245	2	T20810	hypothetical prote
1187	63	5.3	398	2	B70415	proton/sodium-glut	1260	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T20902	hypothetical prote	1261	62.5	5.2	258	2	E91201	type III secretion
1189	63	5.3	411	2	G90154	arsenite transport	1262	62.5	5.2	258	2	A86048	escrt [imported] -
1190	63	5.3	415	2	S39535	corticotropin-rele	1263	62.5	5.2	274	2	AC2946	hypothetical prote
1191	63	5.3	420	2	A57742	cyclin Ia - maize	1264	62.5	5.2	274	2	G98336	sorbitol/mannitol
1192	63	5.3	431	2	T23809	hypothetical prote	1265	62.5	5.2	276	2	G72292	glycerol-3-phospha
1193	63	5.3	448	2	T30982	hypothetical prote	1266	62.5	5.2	276	2	H83568	probable permease
1194	63	5.3	450	2	A34169	alpha-2A-adrenergi	1267	62.5	5.2	280	2	T24579	hypothetical prote
1195	63	5.3	469	2	A82188	hypothetical prote	1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	hypothetical prote	1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	C59095	hypothetical prote	1270	62.5	5.2	293	2	AH0075	probable permease

1271	62.5	5.2	236	2	H83480	cytochrome o ubiq	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	238	2	T37251	homeobox protein c	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	hypothetical prote	1346	62.5	5.2	763	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	A03272	hypothetical prote	1347	62.5	5.2	807	2	T28279	ORF MSV119 probabl
1275	62.5	5.2	333	2	AB1925	hypothetical prote	1348	62.5	5.2	815	2	G97266	mannose-1-phosbat
1276	62.5	5.2	333	2	B89010	protein R08F11.2 [1349	62.5	5.2	837	2	D71027	hypothetical prote
1277	62.5	5.2	335	2	T41426	hypothetical wtf8	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	ABC transporter, p	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	349	2	D97929	hypothetical prote	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	B81450	probable integral	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	358	2	F83829	hypothetical prote	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	F82210	amino acid ABC tra	1355	62.5	5.2	1144	2	AB1983	probable DNA-direc
1283	62.5	5.2	369	2	C88030	protein F46F5.10 [1356	62.5	5.2	1195	2	C87691	hypothetical prote
1284	62.5	5.2	370	2	C69309	conserved hypotet	1357	62.5	5.2	1291	2	T17242	hypothetical prote
1285	62.5	5.2	379	1	S17407	ubiquinol-cytochro	1358	62.5	5.2	1391	2	T20642	hypothetical prote
1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro	1359	62.5	5.2	1397	2	E87998	protein F09C3.1 [i
1287	62.5	5.2	379	2	S58057	ubiquinol-cytochro	1360	62.5	5.2	1576	2	T21172	hypothetical prote
1288	62.5	5.2	382	2	A72373	conserved hypotet	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid	1362	62.5	5.2	1687	2	T43144	vitellogenin II pr
1290	62.5	5.2	383	2	F84771	hypothetical prote	1363	62.5	5.2	1951	2	B43963	RNA viral polymera
1291	62.5	5.2	383	2	T31738	hypothetical prote	1364	62.5	5.2	2150	2	S13553	hypothetical prote
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging	1365	62	5.2	112	2	T11073	NADH2 dehydrogenas
1293	62.5	5.2	391	2	A86632	aromatic amino aci	1366	62	5.2	132	2	D82954	hypothetical prote
1294	62.5	5.2	399	2	H84087	hypothetical prote	1367	62	5.2	174	2	E84028	cell-shape determi
1295	62.5	5.2	404	2	H83249	sodium/glutamate s	1368	62	5.2	175	1	IMECB	colicin B immunity
1296	62.5	5.2	405	1	Q0BE35	BBRF3 protein - hu	1369	62	5.2	198	2	E97217	uncharacterized co
1297	62.5	5.2	406	2	H89006	protein T22F3.11 [1370	62	5.2	201	2	G90134	hypothetical prote
1298	62.5	5.2	409	2	C89942	conserved hypotet	1371	62	5.2	206	2	F89840	conserved hypotet
1299	62.5	5.2	413	2	CT1369	multidrug resistan	1372	62	5.2	209	2	A88656	protein F37C4.1 [i
1300	62.5	5.2	417	2	TS1467	glucose 6 phosphat	1373	62	5.2	209	2	T32573	hypothetical prote
1301	62.5	5.2	420	2	D95018	conserved hypotet	1374	62	5.2	225	2	B65127	type 4 prelin-li
1302	62.5	5.2	420	2	E97891	conserved hypotet	1375	62	5.2	242	1	F75433	probable phosphoes
1303	62.5	5.2	423	2	C70518	probable nanp prot	1376	62	5.2	247	2	AC1332	potassium channel
1304	62.5	5.2	425	2	E97172	flagellin [impor	1377	62	5.2	273	2	E70010	dihydropolamide S
1305	62.5	5.2	426	2	A72080	ct266 hypothetical	1378	62	5.2	285	2	H95943	probable sugar upt
1306	62.5	5.2	426	2	E86542	hypothetical prote	1379	62	5.2	287	2	A69838	transcription regu
1307	62.5	5.2	431	2	H84069	hypothetical prote	1380	62	5.2	288	2	S36953	cytochrome-c oxida
1308	62.5	5.2	440	2	T20092	hypothetical prote	1381	62	5.2	288	2	C83356	probable permease
1309	62.5	5.2	442	1	JQ1042	endothelin recepto	1382	62	5.2	298	2	T29189	hypothetical prote
1310	62.5	5.2	443	2	F30010	NADH2 dehydrogenas	1383	62	5.2	305	2	T43972	hypothetical prote
1311	62.5	5.2	443	2	T08136	probable omega-6 d	1384	62	5.2	306	2	AI0209	probable sugar ABC
1312	62.5	5.2	442	2	C85647	hypothetical prote	1385	62	5.2	306	2	T41290	conserved hypotet
1313	62.5	5.2	452	2	G60787	hypothetical prote	1386	62	5.2	312	2	S48851	chalcone reductase
1314	62.5	5.2	452	2	G64844	probable membrane	1387	62	5.2	312	2	S48849	chalcone reductase
1315	62.5	5.2	455	2	D97217	Glycosyltransferas	1388	62	5.2	315	2	T24821	hypothetical prote
1316	62.5	5.2	457	2	F96562	UDP-N-acetylmuramo	1389	62	5.2	331	2	AB3117	hypothetical prote
1317	62.5	5.2	459	2	AF3284	high-affinity bran	1390	62	5.2	344	2	T05987	hypothetical prote
1318	62.5	5.2	461	2	S57713	probable mannosyl	1391	62	5.2	345	2	T32203	hypothetical prote
1319	62.5	5.2	468	2	A49131	inositol 1,4,5-tri	1392	62	5.2	351	2	C86408	F3H9.12 protein -
1320	62.5	5.2	470	2	C70641	hypothetical prote	1393	62	5.2	352	2	C98170	hypothetical prote
1321	62.5	5.2	487	2	S73161	hypothetical prote	1394	62	5.2	353	2	T42971	hypothetical prote
1322	62.5	5.2	490	2	T40116	hypothetical prote	1395	62	5.2	360	2	A53611	interleukin-8 rece
1323	62.5	5.2	492	2	AC0768	probable transmemb	1396	62	5.2	360	2	T33260	hypothetical prote
1324	62.5	5.2	494	2	T15502	hypothetical prote	1397	62	5.2	362	2	B57641	G protein-coupled
1325	62.5	5.2	501	1	JN0539	head protein gp5 -	1398	62	5.2	370	2	H84111	response regulator
1326	62.5	5.2	502	2	C86263	hypothetical prote	1399	62	5.2	377	2	T05427	hypothetical prote
1327	62.5	5.2	505	2	S44647	f42h10.1 protein -	1400	62	5.2	379	2	S58457	ubiquinol-cytochro
1328	62.5	5.2	507	2	S52677	probable membrane	1401	62	5.2	379	2	E58851	ubiquinol-cytochro
1329	62.5	5.2	546	2	AE0571	probable membrane	1402	62	5.2	381	2	T11440	probable two-compo
1330	62.5	5.2	547	2	S64332	probable membrane	1403	62	5.2	383	2	C95965	bicyclomycin resis
1331	62.5	5.2	568	2	S64567	probable membrane	1404	62	5.2	398	1	E64112	hypothetical prote
1332	62.5	5.2	569	2	T22928	hypothetical prote	1405	62	5.2	399	2	F72417	translocation prot
1333	62.5	5.2	572	2	T11478	NADH2 dehydrogenas	1406	62	5.2	399	2	JC5279	cell-division prot
1334	62.5	5.2	578	2	I56215	interleukin-10 rec	1407	62	5.2	400	2	AB1565	xylose operon regu
1335	62.5	5.2	580	2	T02596	hypothetical prote	1408	62	5.2	402	2	D70186	conserved hypotet
1336	62.5	5.2	601	2	T11451	NADH2 dehydrogenas	1409	62	5.2	403	2	B69338	conserved hypotet
1337	62.5	5.2	608	2	T34391	hypothetical prote	1410	62	5.2	411	2	H72088	protein-tyrosine-p
1338	62.5	5.2	610	2	A28798	myosin-light-chain	1411	62	5.2	432	1	A34845	hypothetical prote
1339	62.5	5.2	621	2	B95897	probable cellulose	1412	62	5.2	432	2	T21880	hypothetical prote
1340	62.5	5.2	638	2	G02068	white homolog - hu	1413	62	5.2	435	2	T47737	hypothetical prote
1341	62.5	5.2	668	2	C71868	hypothetical prote	1414	62	5.2	444	2	F81367	probable transmemb
1342	62.5	5.2	685	2	T04073	intensifier 1 prot	1415	62	5.2	454	2	H65054	hypothetical prote
1343	62.5	5.2	697	2	T19254	hypothetical prote	1416	62	5.2	454	2	H65054	hypothetical prote

A:Gene: CRSP:F26F4.4
A:Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1

Query Match 17.1%; Score 204; DB 2; Length 478;
Best Local Similarity 26.5%; Pred. No. 2.7e-11;
Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;

QY 42 GREKKGISDVRRTFCFLVPTFDLLFVTLWII-----ELNVNGGIENITL 86
DB 69 GSRIGVSKDKRFIVITFTDTSITILLMLLCTVTRDDWDKVFNEINI-----FNP 121
QY 87 EVNQDYSSYDFIFLLAVFRFKVLLIAYAVCLRHWAIALTAVTSALLAKVILSKL 146
DB 122 KFIIRI-----SLFDIVLLAVRLMLILGVVYICILVKQWYTVAFITLASSAYILMKVLFFYN 177
QY 147 FSGAGFYVLPIL--SPLAMIEWTFLDFKVLPOAEENRLLIVQDASRAALIPGLSD 205
DB 178 HSSAVPPLLLITTSFTLWSEFYMLPFOILPRRYARREL-----DGIEN 224
QY 206 GQFYSPPESEA-----GSEEAEEKQDSEK 230
DB 225 PEFSTDDEARSNRRHRRGRQNSGNQSEAP 255

RESULT 3
H90281
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90281
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KUR>
A:Cross-references: UNIPROT:Q97YQ0; GB:AE006641; NID:gl3814471; PIDN:AAK41511.1; GSPDB:G-
C:Genetics:
A:Gene: dppB-1

Query Match 8.6%; Score 102.5; DB 2; Length 348;
Best Local Similarity 23.7%; Pred. No. 0.066;
Matches 49; Conservative 35; Mismatches 66; Indels 57; Gaps 9;

QY 15 SQSHASLRNIHSINPTQLMARIESYEGREKGISDVRTFCFLVPTFDLLFVTLWIIEL 74
DB 46 AQFSQTLFKNAHLNSTQIQIAVEKY--RE-----SLIAAYGL 81
QY 75 NVNGGIENITL-----EVMQDYSSYDFIFLLAVFRFKVLLIAYAVCLRHWAIAL 128
DB 82 N-----QPIIDKVFQIYNLMRFDFGTAYF--LOAPSGSREVSSIAYLEN-----TILL 130
QY 129 TVAVTSALLAKVILSKLFSQGAFA-GVVLPIISFILAMIEWTFLDFKVLPOAEENRLL 187
DB 131 FTTATVIFVAGTITIGLSAKRFEKVIATIAIVHSIPTWMLGF-----VL 178
QY 188 IVQDASRAALIPGLSDGQFYSPPE 214
DB 179 IALAYAVKVPFGMTS---VPPKN 202

RESULT 4
D75080
glucose-1-phosphate thymidyltransferase related protein PAB2433 - Pyrococcus abyssi
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75080
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

[illegible]

T21969
hypothetical protein F38E11.7 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T21969
R/Matthews, P.
submitted to the EMBL Data Library, January 1996
A/Reference number: Z19495
A/Accession: T21969
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-767 <WTL>
A/Cross-references: UNIPROT:Q20170; EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GNO0022; CESP:F38E11
A/Experimental source: clone F38E11
C/Genetics:
A/Genes: CESP:F38E11.7
A/Map position: 4
A/Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 600/2

Query Match 7.2%; Score 86.5; DB 2; Length 767;
Best Local Similarity 24.8%; Pred. No. 5.4;
Matches 35; Conservative 22; Mismatches 49; Indels 35; Gaps 5;

Qy 61 FDLFVTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLIL---AYAV 117
Db 109 FDIILRSMLSFEY---DGLVITSFSTWRHYVHSFPAIDLLAIFPFDYLLIRKTSAAF 164
Qy 118 CRLRHWW-----AIALTTAVTSAPFLAKVILSKLFSQAGFYGYLPI 158
Db 165 CRLNRFLKIYRIANFIAQSYGKLTQVTISLKIPTACFLFHV-----NACVFYIISV 217
Qy 159 ISFILAW--IETWFLDPKVL 177
Db 218 NSDTSSWDGYNATPDDDEYLP 238

RESULT 7
B81299
probable molybdopterin biosynthesis protein Cj1519 [imported] - *Campylobacter jejuni* (str
C/Species: *Campylobacter jejuni*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 16-Aug-2004
C/Accession: B81299
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Accession: B81299
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-396 <PAR>
A/Cross-references: UNIPROT:Q9PMES; GB:AL139078; GB:AL111168; NID:G6968723; PIDN:CAB7393
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Genes: moa2; Cj1519
C/Supfamily: Molybdenum cofactor molybdenum incorporation protein MoeA

Query Match 7.2%; Score 85.5; DB 2; Length 396;
Best Local Similarity 21.0%; Pred. No. 3.1;
Matches 47; Conservative 35; Mismatches 81; Indels 61; Gaps 9;

Qy 4 LPEDMENALTGSSQSHASLRNIHSINPTQLMARIESYEGREKKGISDVRTFTCLF----- 58
Db 185 LGEALENPAQIRSSNHIAIANL-----AKVLNCDTRVFPLLKDEK 225
Qy 59 VTFDPLLVTLWIIELNVNGGIE-----NTLEKEVMQYDYSSYFDI----- 100
Db 226 ATFTLESALQSCDILVTGVMGDFDPLKAIKEYEIIIDKADIKPGRHIKIAKANEX 285
Qy 101 FLAV--FRFVLLIYAVCR--LRHWAIATLTAVTSAPFLAKVILSKLFSQAGFYVL 156
Db 286 FIIALPGFPYSAMVNFNLYREILNSW-----LLQPKDYICKAPLQSSYKKKT 333

Qy 157 PIISFILAWIETWFLDPKVLPO-EAEEENRLLIVQDASERAALI 199
Db 334 PYLEFVACNIE--FKNGRIILANLEGKKKGSSAIINLNKAAALM 375

RESULT 8
A57219
Batten disease-related protein CLN3 - human
C/Species: *Homo sapiens* (man)
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C/Accession: A57219
R/Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler, E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu, J.; Mole, S.E.
Cell 82, 949-957, 1995
A/Title: Isolation of a novel gene underlying Batten disease, CLN3.
A/Reference number: A57219; MUID:96016090; PMID:7553855
A/Accession: A57219
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-438 <LER>
A/Cross-references: UNIPROT:Q13286; GB:U32680; NID:G1039422; PIDN:AAB51075.1; PID:G10394
C/Genetics:
A/Genes: GDB:CLN3
A/Cross-references: GDB:120593; OMIM:204200
A/Map position: 16p12.1-16p11.2
C/Supfamily: CLN3 protein/Battenin/Batten disease protein/BTN1 protein
C/Keywords: membrane protein

Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 3.5;
Matches 38; Conservative 18; Mismatches 46; Indels 47; Gaps 8;

Qy 64 LFVTLWMII-----ELNVNGGI-----ENTLEKEVMQYDYSSYFDIFLLAVRF 108
Db 277 VFKGLLWYIVPLVVYFAEYFINGQLPELFFWNTLSLHAQQYRWYQM---LYQAGVFAS 333
Qy 109 KVILAYAVCRLRHWAIAUTTAVTSAPFLAKVILSKLFSQAGFYGYVPIISFTL----- 163
Db 334 R---SSLRCCIRIFTWALALLQCLNLVFLIADV-----WFGF-LPSIYLVFLIILY 380
Qy 164 -----AWIETWFLDPKVLPOEAEEENR 185
Db 381 EGLLGAAYVNT----FHNIALETSDDEHR 405

RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - *Lyme disease spirochete*
C/Species: *Borrelia burgdorferi* (*Lyme disease spirochete*)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: G70172
R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a *Lyme disease spirochete*, *Borrelia burgdorferi*.
A/Reference number: A70100; MUID:98065943; PMID:9403685
A/Accession: G70172
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-448 <KLE>
A/Cross-references: UNIPROT:O51531; GB:AE001160; NID:G2688505; PIDN:AAB9152
A/Experimental source: strain B31

Query Match 7.1%; Score 85; DB 2; Length 448;
Best Local Similarity 24.4%; Pred. No. 4;
Matches 47; Conservative 28; Mismatches 64; Indels 54; Gaps 11;

Qy 50 DVRTFTCLFVTFDPLLVTL-----LWIIELNVNGGIE-NTLEKEVMQYDYSS-----Y 97
Db 271 DTHKYAAYSISFSIYFIIFNIHSFCSISLNMGYEMHNSKKIMKVAIYLSKIGLKLA 330

QY 98 FDIFFLAVERFKVLIILAYAVCLRLRHWAIALTTAVTSAFLLAKVI--LSKLFSGQA-----151
Db 331 LTSFVLFIFFPAPYFYTL-KYSHLIGIILRYSSVSAPFMALAFQVLFGLFFRAGASPSF 389
QY 152 -----FGYVLPISFILAMIEWFLDFKVLPOAEENLLIV-----QDASERAA 197
Db 390 GAIMEGVSFTVYTIP-IAFVLA-----NYTNLPPE-----IIVFIPSLDAIKLVV 434
QY 198 LIPGGLSDGOFYS 210
Db 435 SLP-----YFYS 441
RESULT 10
A41680
Integral membrane protein pssa - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
C;Accession: A41680
R;Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A;Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synthetase
A;Reference number: A41680; MUID:92084729; PMID:1748687
A;Accession: A41680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <KUG>
A;Cross-references: GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01084.1; PID:d1001553; PID:g12882
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3
C;Keywords: membrane protein
Query Match 7.1%; Score 84.5; DB 2; Length 471;
Best Local Similarity 24.4%; Pred. No. 4.7;
Matches 32; Conservative 22; Mismatches 38; Indels 39; Gaps 7;
QY 55 FCLFVTFLDLFVTLIIELNVNGIENLEKEVMQY-----DYSSYDFIFLLAV 105
Db 117 FLLFLNFEQVKSVMW-LDPNLRVA---TREADIMEYAVNCHVITWERIVSHDFIFAFGH 172
QY 106 F-----RFKVLILAYAVCLRLRHWAIALTTAVTSAFLLAKVLSKLFSGAGFYVLPISF 161
Db 173 FWGWAKALLIRSYGLC-----WTISITWELTELF-----FMHLLP--NF 210
QY 162 ILAMIEWFLD 172
Db 211 AECWWDQVILD 221
RESULT 11
H97002
Probable integral membrane protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97002
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q97KT1; GB:AE001437; PIDN:AAK7811.1; PID:g15023727; GSPDB:C
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0835
Query Match 7.0%; Score 83.5; DB 2; Length 352;
Best Local Similarity 19.2%; Pred. No. 4.1;
Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

QY 38 ESYEGREKGISDVRTFCLFVTFD-----LLFVTLIIIEL 74
Db 115 EFINVRDKTNDKMLIKAYLVQNKTLNMRIVKDEQIGGLSKSERITAFATVLIITS 174
QY 75 NVNGGI-----ENTLEKEVMQ-----YDYSSYDFIF-----LLAVFRFKVL 111
Db 175 VNGAVIIRDRNTYRYMYSPNSKFEVIFGNVIYNYIFSIQLFIANSMAIFGIYIG 234
QY 112 I-----LAYAVCLRLRHWAIALTTAVTSAF-----LLAKVLSKLFSGAGFYVLPISF 160
Db 235 ISFLKMLSYGL-----ILTLVMTFTFGTIVCFIKENKELVANNFSA-----IS 276
QY 161 FILAMIEWFLDFKVLPO 178
Db 277 LILSLVGGTFINIKIMPE 294
RESULT 12
AE0302
sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0302
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, H. Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <KUR>
A;Cross-references: UNIPROT:Q8ZDT0; GB:AL590842; PIDN:CAC91281.1; PID:gl5980470; GSPDB:G
C;Genetics:
A;Gene: YPO2476
C;Superfamily: inner membrane protein ucpa
Query Match 6.9%; Score 83; DB 2; Length 291;
Best Local Similarity 22.3%; Pred. No. 3.7;
Matches 44; Conservative 26; Mismatches 57; Indels 70; Gaps 10;
QY 46 KGISDVRRFCLFVTFDFFLLFVTLIIELNVN-----GGIENTL-----84
Db 9 KQGVSLAASLYGYSIFWFYPIFWLAVLSLTWRVFGVPTFNGLNFIILVMQDPLFWKS 68
QY 85 EKEVMQDYSSYDFIFLLAVFRFKVLIILAYAVCLRLRHWAIALTTAVTSAFLLAKV---141
Db 69 MLNVMRFLMY--YLPVIFISSFLF-----AFGLQKLKHG-----RTFVALSFLLANVSSG 116
QY 142 -----ILSKLFSGQA-----FGYVLPISF-----FILAMIEW-----FL 171
Db 117 VAYSIVFSKIFSQNGPLNTFLYDWFGLTFLPWLTSDFAMLSIALVLTWTKFVGYGVLIFS 176
QY 172 DFKVLPOE-----AEEEN 184
Db 177 GLNSIPKEIYSAEELDN 193
RESULT 13
S34960
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion
C;Species: mitochondrion Crithidia oncopelti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34960
R;Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S34958
A;Accession: S34960
A;Molecule type: DNA
A;Residues: 1-590 <MAS>
A;Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CAA39492.1; PID:g12882
C;Genetics:

A;Gene: NDS
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 6.9%; Score 83; DB 1; Length 590;
Best Local Similarity 23.9%; Pred. No. 8.4; Indels 42; Gaps 7;
Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;
Qy 55 FCLFVTF-----DLT-----FTLLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVF 106
Db 95 FILFYAFYMYDLMKRFNIFWVFLCNFFI-----LSYDYLTAVCWELLGLF 146
Qy 107 RFKVLILAYAVCRLRHWAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFILAWI 166
Db 147 SF--FLISY-----FWYRFALKFGKSPFISKI-----GDVLLLLSFVMTFI 187
Qy 167 ET-----WFLDF 173
Db 188 STGYGMINFYFVNF 201

RESULT 14
B29835
TraS protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1998 #sequence_revision 04-Aug-1998 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncP-
A;Reference number: A29835; MUID:86223783; PMID:3011738
A;Accession: B29835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
A;Cross-references: UNIPROT:P14498
C;Genetics:
A;Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;
Best Local Similarity 23.8%; Pred. No. 2.4; Indels 35; Gaps 6;
Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;
Qy 61 FDLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLL-----AVFRFKVLILAY 115
Db 44 FQLLFI----IFDIFINSVR-----DYH--YFDTFVITLGSNAFFSLVFLMSTY 87
Qy 116 AVCRLRHWAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPII-----SFLAW 165
Db 88 NLVSLK----ISLSEITEQSLLKLVERKINSYQFLMVVNAIVGCVLLSSGGRFVAGL 143
Qy 166 IETWFELDPKV 175
Db 144 GFSWFVTYLI 153

RESULT 15
C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Praser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
C;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; GB:U39703; GB:L43967; NID:G3844835; PIDN:AAC71467.1;
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ygiH protein
Query Match 6.9%; Score 82.5; DB 1; Length 239;
Best Local Similarity 21.7%; Pred. No. 3.3; Indels 39; Gaps 8;
Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;
Qy 42 GREKKGISDVRRTF-----CLFVTFDLFLFTLL-WIIELVNNGGIENTLEKEVMQYD 92
Db 42 GSKNPATNSMRVFGKIGFLVAIFDAKGFPAFLTWIL---PRFGLQGYLTKVYQST 98
Qy 93 YYSYFDIFLLAV-----FRPK-----VLILAYAVCRLRHWNAI-----ALTAVTSA 135
Db 99 YFLSYLSCPAATIGHIPPLYFKFKGKAIAATGGSLLAISLWFLICLLIWIIMITLITKY 158
Qy 136 FLLAKVILSKLFSQAGFYVLPPIISFILAWIE 167
Db 159 VSLASLITF-----FVLAVI-ILIPWLD 180

Search completed: January 24, 2005, 16:14:54
Job time : 73 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 16:04:45 ; Search time 193 Seconds

(without alignments)
697.604 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

Sequence: 1 MNHLPDMENALGSSQSSHA.....EAGSEBAEEKQDSEKPLEL 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1195	100.0	234	1	MENT_HUMAN
2	1134.5	94.9	235	1	MENT_MOUSE
3	796	66.6	227	2	Q6DI38
4	700.5	58.6	448	2	Q6DFR7
5	698.5	58.5	444	2	Q6PFA0
6	698.5	58.5	444	2	AAH57738
7	684	57.2	448	2	Q6GNT3
8	664	55.6	445	1	ML64_HUMAN
9	664	55.6	445	2	AAP35610
10	656.5	54.9	446	1	ML64_MOUSE
11	656.5	54.9	446	2	BAC30977
12	632	52.9	448	2	Q6PH03
13	632	52.9	448	2	AAH56766
14	492	41.2	107	2	Q8BMP8
15	348	29.1	568	2	Q7QIT3
16	343	28.7	545	2	Q8MZH4
17	343	28.7	545	2	AAS64770
18	343	28.7	583	2	Q9W145
19	343	28.7	583	2	AAR19767
20	343	28.7	583	2	AAF47232
21	204	17.1	447	2	Q19819
22	104.5	8.7	294	1	ML64_SALFO
23	102.5	8.6	348	2	Q97YQ0
24	93.5	7.8	424	2	Q9UZW1
25	93.5	7.8	564	2	Q8HQ10
26	91	7.6	246	2	Q8DU10
27	91	7.6	525	2	Q7VFT4
28	91	7.6	651	2	Q8DZX0
29	91	7.6	651	2	Q8ESM0
30	90.5	7.6	262	2	Q7NB74
31	90	7.5	1911	2	O02038

32	89.5	7.5	233	2	Q6JCT3	Q6jct3 aleurodicus
33	89.5	7.5	367	2	Q8HEH8	Q8heh8 varroa dest
34	89.5	7.5	376	2	Q6JCT6	Q6jct6 aleurodicus
35	89.5	7.5	488	2	Q840W7	Q840w7 streptococc
36	89	7.4	373	2	Q7RTB5	Q7rtb5 plasmodium
37	88.5	7.4	384	2	Q6WNV4	Q6wnv4 rana catesb
38	88.5	7.4	384	2	AAQ22365	AAq22365 rana cate
39	87	7.3	610	2	Q7RRS2	Q7rrs2 plasmodium
40	87	7.3	707	2	Q6GN42	Q6gn42 xenopus lae
41	87	7.3	720	2	Q8PYM2	Q8pym2 methanosarc
42	86.5	7.2	328	2	Q7NLL9	Q7nll9 gloeobacter
43	86.5	7.2	605	2	Q7Z205	Q7z205 caenorhabdi
44	86.5	7.2	891	2	Q8JLA2	Q8jla2 ectromelia
45	86.5	7.2	1204	2	Q8SOC3	Q8soc3 oryza sativ
46	86	7.2	1050	2	Q87LG6	Q87lg6 neurospora
47	86	7.2	1056	2	Q7S7L6	Q7s7l6 neurospora
48	85.5	7.2	174	2	P97067	P97067 salmonella
49	85.5	7.2	336	2	Q95086	Q95086 homo sapien
50	85.5	7.2	339	2	Q95089	Q95089 homo sapien
51	85.5	7.2	336	2	Q9PME5	Q9pme5 campylobact
52	85.5	7.2	438	1	CLN3_HUMAN	CLN386 homo sapien
53	85.5	7.2	438	2	AAAD01555	AAad01555 homo sapi
54	85.5	7.2	473	1	PSS1_HUMAN	P48651 homo sapien
55	85.5	7.2	747	2	Q93GL8	Q93gl8 salmonella
56	85	7.1	348	2	Q9SF17	Q9sf17 arabidopsis
57	85	7.1	377	2	Q6I2C1	Q6i2c1 bacillus an
58	85	7.1	448	2	O51S31	O51s31 borrelia bu
59	85	7.1	797	2	Q82GJ8	Q82gj8 streptomyce
60	84.5	7.1	471	1	PSS1_CRILO	Q00576 cricetus
61	84.5	7.1	473	1	PSS1_MOUSE	Q991b2 mus musculu
62	84.5	7.1	892	2	Q9JF90	Q9jf90 vaccinia vi
63	84	7.0	469	2	Q9HJK8	Q9hjk8 thermoplas
64	84	7.0	493	2	Q7TSH7	Q7tsh7 mus musculu
65	84	7.0	1700	2	Q75JN1	Q75jn1 dictyosteli
66	84	7.0	1700	2	AAS38702	Aas38702 dictyoste
67	83.5	7.0	275	2	Q8XIT3	Q8xit3 clostridium
68	83.5	7.0	303	2	Q6FNB8	Q6fnb8 candida gla
69	83.5	7.0	322	2	Q8L840	Q8lb40 arabidopsis
70	83.5	7.0	352	2	Q97KT1	Q97kt1 clostridium
71	83.5	7.0	355	2	Q6KI24	Q6ki24 mycoplasma
72	83.5	7.0	355	2	AAT27752	Aat27752 mycoplas
73	83.5	7.0	380	2	Q97C55	Q97c55 thermoplas
74	83.5	7.0	490	2	Q9CTA9	Q9cta9 mus musculu
75	83.5	7.0	599	2	Q6PCK2	Q6pcx2 mus musculu
76	83.5	7.0	599	2	AAH59080	Aah59080 mus muscu
77	83.5	7.0	662	2	Q88P20	Q88p20 pseudomonas
78	83.5	7.0	834	2	Q9JHF5	Q9jhf5 mus musculu
79	83.5	7.0	834	2	Q9JL12	Q9jll2 mus musculu
80	83.5	7.0	834	2	Q91W06	Q91w06 mus musculu
81	83.5	7.0	1034	2	Q7Z2B9	Q7z2b9 trypanosoma
82	83	6.9	238	2	Q6YR96	Q6yr96 onion yello
83	83	6.9	238	2	BAD04204	Bad04204 onion yel
84	83	6.9	248	2	Q8GCS6	Q8gcs6 eubacterium
85	83	6.9	291	2	Q82DT0	Q82dt0 yersinia pe
86	83	6.9	291	2	AAS62501	Aas62501 yersinia
87	83	6.9	589	2	Q7TWM1	Q7tmw1 mus musculu
88	83	6.9	590	2	Q34192	Q34192 crithidia o
89	83	6.9	1056	2	Q8C2V1	Q8c2v1 mus musculu
90	83	6.9	2661	2	Q7RMS4	Q7rms4 plasmodium
91	82.5	6.9	174	2	P97231	P97231 salmonella
92	82.5	6.9	186	1	TRS2_ECOLI	TRs2 escherichia
93	82.5	6.9	186	2	Q7BBW2	Q7bbw2 salmonella
94	82.5	6.9	186	2	AAH90724	Aam90724 salmonell
95	82.5	6.9	239	1	Y247_MYCGE	Y24789 mycoplasma
96	82.5	6.9	341	2	Q56918	Q56918 yersinia en
97	82.5	6.9	367	2	Q8HCK3	Q8hck3 varroa dest
98	82.5	6.9	406	2	Q87249	Q87249 lactococcus
99	82.5	6.9	419	2	O19134	O19134 cryptocolagus
100	82.5	6.9	471	2	Q9QW77	Q9qw77 cricetus
101	82.5	6.9	510	2	Q950M6	Q950m6 rhizophydiu
102	82.5	6.9	604	2	Q8RHJ3	Q8rhj3 fusobacteri
103	82.5	6.9	717	1	TRD1_ECOLI	TRd1 escherichia
104	82.5	6.9	717	2	O87742	O87742 escherichia

105	82.5	6.9	739	2	AAC44181	Aac44181 escherich	178	80.5	6.7	732	2	Q6SIZ5	Q6siz5 escherichia
106	82.5	6.9	891	2	O57223	O57223 vaccinia vi	179	80.5	6.7	732	2	AAR25112	Aar25112 escherich
107	82.5	6.9	891	2	O6J3A9	O6j3a9 vaccinia vi	180	80.5	6.7	738	1	TRD2_ECOLI	P22708 escherichia
108	82.5	6.9	891	2	O80DW2	O80dw2 cowpox viru	181	80.5	6.7	738	2	Q7AK52	Q7ak62 plasmid r10
109	82.5	6.9	891	2	AAT10519	Aat10519 vaccinia	182	80.5	6.7	738	2	BAAT78884	Baa78884 plasmid r
110	82.5	6.9	892	2	O6RZH3	O6rzh3 rabbitpox v	183	80.5	6.7	891	1	VP4A_VACCC	P20642 vaccinia vi
111	82.5	6.9	892	2	AAS49831	Aas49831 rabbitpox	184	80.5	6.7	891	1	VP4A_VACCV	P16715 vaccinia vi
112	82.5	6.9	894	2	O8QMU0	O8qmu0 cowpox viru	185	80.5	6.7	891	2	Q76ZQ5	Q76zq5 vaccinia vi
113	82.5	6.9	1022	2	O88V00	O88v00 lactobacill	186	80.5	6.7	891	2	Q8V4W5	Q8v4w5 monkeypox v
114	82	6.9	156	2	O81501	O81501 hepatitis c	187	80.5	6.7	891	2	AO89408	Aao89408 vaccinia
115	82	6.9	301	2	O8RLZ3	O8rlz3 haemophilus	188	80.5	6.7	1887	2	Q7SC49	Q7sc49 neurospora
116	82	6.9	303	2	O89L18	O89l18 brachyrihizob	189	80.5	6.7	1780	2	Q9ZT82	Q9zt82 arabidopsis
117	82	6.9	472	2	Q70J50	Q70j50 haemophilus	190	80	6.7	103	2	Q9RX39	Q9rx39 deinococcus
118	82	6.9	472	2	CAE18174	Caer18174 haemophil	191	80	6.7	156	2	Q81513	Q81513 hepatitis c
119	82	6.9	587	2	Q6C0H8	Q6c0h8 yarrowia li	192	80	6.7	197	2	Q7YWX2	Q7ywx2 caenorhabdi
120	82	6.9	589	1	RGPI_MOUSE	R46061 mus musculu	193	80	6.7	238	2	Q95KH1	Q95kh1 macaca fasc
121	82	6.9	589	2	O6NZB5	O6nzb5 mus musculu	194	80	6.7	255	2	Q6V7H6	Q6v7h6 equine arse
122	82	6.9	589	2	O8C2E3	O8c2e3 mus musculu	195	80	6.7	255	2	AAR14206	Aar14206 equine ar
123	82	6.9	589	2	Q8C2E3	Q8c2e3 mus musculu	196	80	6.7	280	2	Q6HEF5	Q6hef5 bacillus th
124	82	6.9	589	2	Q81YS2	Q81ys2 mus musculu	197	80	6.7	280	2	Q731V3	Q731v3 bacillus ce
125	82	6.9	589	2	AAH66213	Aah66213 mus muscu	198	80	6.7	280	2	Q819H0	Q819h0 bacillus ce
126	82	6.9	646	2	Q6ZPH4	Q6zph4 mus musculu	199	80	6.7	280	2	Q81MM0	Q81mm0 bacillus an
127	82	6.9	646	2	BAC98262	Bac98262 mus muscu	200	80	6.7	280	2	AAS42964	Aas42964 bacillus
128	82	6.9	647	2	O8PXU3	O8pxu3 methanosarc	201	80	6.7	290	2	Q99UM2	Q99um2 staphylococ
129	82	6.9	989	2	O6CDE6	O6cde6 yarrowia li	202	80	6.7	290	2	Q7A5Y6	Q7a5y6 staphylococ
130	82	6.9	1031	2	P81564	P81564 plasmodium	203	80	6.7	300	2	Q9C840	Q9c840 arabidopsis
131	82	6.9	1466	2	P78576	P78576 emericella	204	80	6.7	300	2	Q7USB9	P40113 saccharomyc
132	81.5	6.8	190	2	Q9KIA9	Q9kia9 escherichia	205	80	6.7	309	1	RTM1_YEAST	Q7usb9 rhodospirell
133	81.5	6.8	297	2	Q9B893	Q9b893 schistosoma	206	80	6.7	343	2	Q7J3A5	Q7j3a5 treponema d
134	81.5	6.8	311	2	Q8CD14	Q8cd14 mus musculu	207	80	6.7	347	2	Q9FFM1	Q9ffm1 arabidopsis
135	81.5	6.8	349	1	RNFD_PASMU	Q9cnp3 pasteurella	208	80	6.7	355	2	Q73J45	Q73j45 treponema d
136	81.5	6.8	352	2	Q9H7E5	Q9h7e5 homo sapien	209	80	6.7	355	2	AAS13187	Aas13187 treponema
137	81.5	6.8	387	2	Q72CJ7	Q72cj7 desulfovibr	210	80	6.7	359	2	Q7N4F8	Q7n4f8 photorhabdu
138	81.5	6.8	387	2	AAS95764	Aas95764 deaulfovi	211	80	6.7	360	2	Q9H1X3	Q9h1x3 homo sapien
139	81.5	6.8	414	2	O6PAH4	O6pah4 mus musculu	212	80	6.7	360	2	O58427	O58427 pyrococcus
140	81.5	6.8	414	2	AAH60306	Aah60306 mus muscu	213	80	6.7	360	2	Q6FXI7	O6fxi7 candida gla
141	81.5	6.8	438	2	Q35934	Q35934 mus musculu	214	80	6.7	540	2	Q759Y6	Q759y6 ashbya goss
142	81.5	6.8	438	2	O8C5B1	O8c5b1 mus musculu	215	80	6.7	661	2	AAS52057	Aas52057 ashbya go
143	81.5	6.8	438	2	AAH58753	Aah58753 mus muscu	216	80	6.7	661	2	Q7VH08	Q7vh08 helicobacte
144	81.5	6.8	447	2	Q7VR00	Q7vr00 candidatus	217	80	6.7	700	2	Q720Z1	Q720z1 listeria mo
145	81.5	6.8	465	2	Q803C9	Q803c9 brachydanio	218	80	6.7	700	2	AAT03873	Aat03873 listeria
146	81.5	6.8	519	2	Q9NV58	Q9nv58 homo sapien	219	80	6.7	3010	2	Q9QIY9	Q9qi9 hepatitis c
147	81.5	6.8	577	2	O6PI26	O6pi26 homo sapien	220	79.5	6.7	269	2	AAT03604	Aat03604 listeria
148	81.5	6.8	577	2	Q7Z748	Q7z748 homo sapien	221	79.5	6.7	269	2	AAAT03604	Q89nc2 brachyrihizob
149	81.5	6.8	577	2	AAH17274	Aah17274 homo sapi	222	79.5	6.7	307	2	Q89NC2	Q8esy3 oceanorhizob
150	81.5	6.8	577	2	AAH47879	Aah47879 homo sapi	223	79.5	6.7	367	2	Q89SY3	Q8esy3 oceanorhizob
151	81.5	6.8	577	2	Q8DLB4	Q8dlb4 synechococc	224	79.5	6.7	391	2	Q6TV96	Aatv96 xiphinema a
152	81.5	6.8	892	2	Q775R6	Q775r6 camelipox vi	225	79.5	6.7	391	2	AAQ75776	Aaq75776 xiphinema
153	81.5	6.8	892	2	Q8V2P5	Q8v2p5 camelipox vi	226	79.5	6.7	438	1	CLN3_CANFA	Q29611 canis fami
154	81.5	6.8	1092	2	Q755K6	Q755k6 ashbya goss	227	79.5	6.7	463	2	Q92E13	Q92e13 listeria in
155	81.5	6.8	1092	2	AA53185	Aa53185 ashbya go	228	79.5	6.7	488	2	Q6QU70	Q6qu70 aspergillus
156	81.5	6.8	1480	2	Q7R386	Q7r386 giardia lam	229	79.5	6.7	488	2	AAS66784	Aas66784 aspergill
157	81	6.8	385	2	Q9ZQ69	Q9zq69 arabidopsis	230	79.5	6.7	491	1	VIE1_HCMVT	P03169 human cytom
158	81	6.8	410	2	Q6D043	Q6d043 erwinia car	231	79.5	6.7	546	1	FVR2_RAT	P06815 rattus norv
159	81	6.8	520	1	YH07_CABEL	Yh07cabel	232	79.5	6.7	546	1	Q51954	O51954 borrelia he
160	81	6.8	532	1	YH07_YEAST	Yh07yeast	233	79.5	6.7	598	2	Q6BZ08	Q6bz08 debaryomyce
161	81	6.8	805	2	Q8XSV5	Q8xsv5 talstonia s	234	79.5	6.7	674	2	Q86P19	Q86p19 drosophila
162	81	6.8	3010	2	Q8QR18	Q8qr18 hepatitis c	235	79.5	6.7	726	2	Q9EUI3	Q9euj3 salmonella
163	80.5	6.7	174	2	P97066	P97066 salmonella	236	79.5	6.7	784	2	Q9VYV0	Q9vyy0 drosophila
164	80.5	6.7	242	2	Q8TNE9	Q8tnes methanosarc	237	79.5	6.7	784	2	Q8VDB0	Q8vdb0 chlorobium
165	80.5	6.7	322	2	Q9SNE5	Q9snes arabidopsis	238	79.5	6.7	3409	2	Q7S127	Q7s127 neurospora
166	80.5	6.7	353	1	ML1A_PHOSU	P49217 phodopus su	239	79	6.6	114	2	Q6VRR6	Q6vrr6 helicobacte
167	80.5	6.7	366	2	Q86K58	Q86k58 dictyosteli	240	79	6.6	114	2	AAAR03870	Aar03870 helicobac
168	80.5	6.7	396	2	Q9US09	Q9us09 schizosacch	241	79	6.6	251	2	Q6M012	Q6m012 methanococc
169	80.5	6.7	417	1	TNAB_PROVU	P28785 proteus vul	242	79	6.6	251	2	CAF29844	Caf29844 methanoco
170	80.5	6.7	463	2	Q8Y988	Q8y988 listeria mo	243	79	6.6	300	2	Q80ZK3	Q80zh3 arvicanthis
171	80.5	6.7	463	2	Q722Q4	Q722q4 listeria mo	244	79	6.6	308	2	Q8RGM6	Q8rgm6 fusobacteri
172	80.5	6.7	463	2	AAAT03457	Aat03457 listeria	245	79	6.6	312	2	Q6KH29	Q6kx29 mycoplasma
173	80.5	6.7	486	2	Q9G861	Q9g861 malawimonas	246	79	6.6	323	2	AAT28102	Aat28102 drosophil
174	80.5	6.7	536	1	MYIN_CHLTR	Q46378 chlamydia t	247	79	6.6	323	2	Q7KSI9	Q7ks19 mycoplasma
175	80.5	6.7	548	2	Q7RC45	Q7rc45 plasmodium	248	79	6.6	349	1	AAAI3630	Aai13630 drosophil
176	80.5	6.7	599	2	Q91ME6	Q91me6 human rotav	249	79	6.6	349	1	RNFD_BUCAP	O8ka19 buchnera ap
177	80.5	6.7	644	1	YNL5_YEAST	P53925 saccharomyc	250	79	6.6	356	2	Q7MG43	Q7mg43 vibrio vuln

251	79	6.6	375	2	Q887L9	Q887L9 pseudomonas	324	77.5	6.5	491	2	Q28284	O28284 archaeoglob
252	79	6.6	484	2	Q6NIE0	Q6NIE0 corynebacte	325	77.5	6.5	491	2	Q6SX10	Q6SX10 human cyt
253	79	6.6	484	2	CAB49353	CAB49353 corynebacte	326	77.5	6.5	491	2	AAR31332	AAR31332 human cyt
254	79	6.6	1531	2	Q961L95	Q961L95 homo sapien	327	77.5	6.5	512	2	Q8YGI2	Q8YGI2 brucella me
255	79	6.6	1679	2	Q86TB3	Q86TB3 homo sapien	328	77.5	6.5	556	2	Q89180	Q89180 variola vir
256	79	6.6	3010	2	Q9J3H8	Q9J3H8 hepatitis c	329	77.5	6.5	556	2	Q89232	Q89232 variola vir
257	79	6.6	3010	2	Q9J3H8	Q9J3H8 hepatitis c	330	77.5	6.5	567	2	Q7RNK0	Q7RNK0 plasmodium
258	78.5	6.6	229	1	Y247_MYCPN	Y247_MYCPN mycoplasma	331	77.5	6.5	620	2	Q8EKA1	Q8EKA1 shewanella
259	78.5	6.6	269	2	Q92DL5	Q92DL5 listeria in	332	77.5	6.5	734	1	NUSC_ORYSA	NUSC_ORYSA oryza sativ
260	78.5	6.6	313	2	Q91L0B3	Q91L0B3 streptomyce	333	77.5	6.5	892	1	VP4A_VARV	VP4A_VARV variola vir
261	78.5	6.6	358	1	RNFD_HABIN	RNFD_HABIN haemophilus	334	77.5	6.5	892	2	Q9QNI0	Q9QNI0 variola min
262	78.5	6.6	380	2	Q8A0F8	Q8A0F8 haemophilus	335	77.5	6.5	979	2	Q7MLV5	Q7MLV5 vibrio vuln
263	78.5	6.6	471	1	SH2A_CRIGR	SH2A_CRIGR cricetulus	336	77.5	6.5	1476	2	Q8ST66	Q8ST66 dictyosteli
264	78.5	6.6	512	2	Q8G1D7	Q8G1D7 brucella su	337	77.5	6.5	1784	2	Q25377	Q25377 loligo opal
265	78.5	6.6	666	2	Q8DZL1	Q8DZL1 streptococ	338	77.5	6.5	2141	2	Q869H2	Q869H2 lymphaea sta
266	78.5	6.6	678	2	Q61710	Q61710 mus musculu	339	77	6.4	170	2	Q72UC4	Q72UC4 leptospira
267	78.5	6.6	681	2	Q769F3	Q769F3 homo sapien	340	77	6.4	170	2	Q8FOQ4	Q8FOQ4 leptospira
268	78.5	6.6	681	2	BAC98410	BAC98410 homo sapi	341	77	6.4	170	2	AAS69354	AAS69354 leptospir
269	78.5	6.6	683	2	Q769P4	Q769P4 homo sapien	342	77	6.4	255	2	Q98VN5	Q98VN5 equine arte
270	78.5	6.6	683	2	BAC98409	BAC98409 homo sapi	343	77	6.4	286	2	Q6I082	Q6I082 bacillus an
271	78.5	6.6	766	1	ABC9_HUMAN	ABC9_HUMAN homo sapien	344	77	6.4	286	2	Q73A28	Q73A28 bacillus ce
272	78.5	6.6	769	2	Q6P2Q0	Q6P2Q0 homo sapien	345	77	6.4	286	2	AAS40882	AAS40882 bacillus
273	78.5	6.6	769	2	AAG4384	AAG4384 homo sapi	346	77	6.4	332	2	Q9XTH3	Q9XTH3 caenorhabdi
274	78.5	6.6	987	2	BAC40536	BAC40536 mus muscu	347	77	6.4	353	1	ML1A_MOUSE	ML1A_MOUSE mus musculu
275	78.5	6.6	6473	2	Q8IKH9	Q8IKH9 plasmodium	348	77	6.4	379	2	Q8WEK6	Q8WEK6 thomomys ta
276	78	6.5	188	2	Q81YM2	Q81YM2 bacillus an	349	77	6.4	383	2	Q8TZC2	Q8TZC2 methanopyru
277	78	6.5	188	2	AAT32629	AAT32629 bacillus	350	77	6.4	386	2	Q7MXQ0	Q7MXQ0 porphyromon
278	78	6.5	219	2	Q8W2Y0	Q8W2Y0 oryza sativ	351	77	6.4	419	2	P94949	P94949 methanopyru
279	78	6.5	226	2	Q7R2Y0	Q7R2Y0 avian infec	352	77	6.4	423	2	Q71XS8	Q71XS8 listeria mo
280	78	6.5	240	2	Q9CP66	Q9CP66 pasteurella	353	77	6.4	423	2	AAT04887	AAT04887 listeria
281	78	6.5	245	2	P94625	P94625 clostridium	354	77	6.4	430	2	Q8U1Z6	Q8U1Z6 pyrococcus
282	78	6.5	259	2	Q9KDL3	Q9KDL3 bacillus ha	355	77	6.4	435	2	Q73RD9	Q73RD9 treponema d
283	78	6.5	321	2	Q96XK4	Q96XK4 sulfolobus	356	77	6.4	435	2	AAS10648	AAS10648 treponema
284	78	6.5	339	2	Q8D4K9	Q8D4K9 vibrio vuln	357	77	6.4	444	2	Q6GD70	Q6GD70 staphylococ
285	78	6.5	360	2	Q951A3	Q951A3 tetrahymena	358	77	6.4	444	2	O8NXX5	O8NXX5 staphylococ
286	78	6.5	382	2	Q97HC3	Q97HC3 clostridium	359	77	6.4	490	2	O14670	O14670 homo sapien
287	78	6.5	414	2	Q8TM61	Q8TM61 methanosarc	360	77	6.4	491	2	Q9T251	Q9T251 phytophthor
288	78	6.5	428	2	Q8DSY9	Q8DSY9 vibrio vuln	361	77	6.4	519	2	Q9ASQ7	Q9ASQ7 arabidopsis
289	78	6.5	431	2	Q9JRS0	Q9JRS0 actinobacil	362	77	6.4	559	2	Q9AAX4	Q9AAX4 caulobacter
290	78	6.5	442	2	Q7MD08	Q7MD08 vibrio vuln	363	77	6.4	590	1	NUSM_TRYBB	NUSM_TRYBB trypanosoma
291	78	6.5	471	1	Y872_HABIN	Y872_HABIN haemophilus	364	77	6.4	650	2	Q6G633	Q6G633 staphylococ
292	78	6.5	486	2	Q6HMA8	Q6HMA8 bacillus th	365	77	6.4	650	2	Q6GDG1	Q6GDG1 staphylococ
293	78	6.5	545	2	Q6FSM9	Q6FSM9 candida gla	366	77	6.4	650	2	O8NUK4	O8NUK4 staphylococ
294	78	6.5	641	2	Q9LIC2	Q9LIC2 arabidopsis	367	77	6.4	650	2	Q99QZ7	Q99QZ7 staphylococ
295	78	6.5	650	2	Q7QC08	Q7QC08 anopheles g	368	77	6.4	650	2	Q7A374	Q7A374 staphylococ
296	78	6.5	688	2	Q98M77	Q98M77 rhizobium l	369	77	6.4	738	2	O8L838	O8L838 arabidopsis
297	78	6.5	1297	2	Q9Y817	Q9Y817 schizosacch	370	77	6.4	738	2	AAQ56779	AAQ56779 arabidops
298	78	6.5	2136	1	YCF2_MARPO	YCF2_MARPO marchantia	371	77	6.4	789	1	FTSK_STAAN	FTSK_STAAN staphylococ
299	78	6.5	7180	1	RIAB_CVMJH	RIAB_CVMJH replicase	372	77	6.4	789	2	Q6G9T7	Q6G9T7 staphylococ
300	77.5	6.5	176	2	Q976T7	Q976T7 sulfolobus	373	77	6.4	836	2	Q721P2	Q721P2 plasmodium
301	77.5	6.5	190	2	Q9K1A8	Q9K1A8 escherichia	374	77	6.4	877	2	Q750H8	Q750H8 ashbya goss
302	77.5	6.5	263	2	Q73DX2	Q73DX2 bacillus ce	375	77	6.4	877	2	AAS54463	AAS54463 ashbya go
303	77.5	6.5	263	2	O81183	O81183 bacillus ce	376	77	6.4	991	2	O81330	O81330 arabidopsis
304	77.5	6.5	263	2	AAS39523	AAS39523 bacillus	377	77	6.4	1024	2	Q721P1	Q721P1 plasmodium
305	77.5	6.5	269	2	Q8Y8T5	Q8Y8T5 listeria mo	378	77	6.4	1024	2	O8IKZ6	O8IKZ6 plasmodium
306	77.5	6.5	270	2	O8HIY1	O8HIY1 perognathus	379	77	6.4	1025	2	Q25693	Q25693 plasmodium
307	77.5	6.5	270	2	O8HIY2	O8HIY2 perognathus	380	77	6.4	1117	2	O9M133	O9M133 arabidopsis
308	77.5	6.5	270	2	O8HIY3	O8HIY3 perognathus	381	77	6.4	1477	2	Q6FTFR	Q6FTFR candida gla
309	77.5	6.5	270	2	O8HIY4	O8HIY4 perognathus	382	77	6.4	1500	2	Q9ZU84	Q9ZU84 arabidopsis
310	77.5	6.5	294	2	O8ET10	O8ET10 oceanobacil	383	77	6.4	3010	2	Q81757	Q81757 hepatitis c
311	77.5	6.5	299	2	Q8ZAIL	Q8ZAIL yersinia pe	384	77	6.4	3010	2	O81757	O81757 hepatitis c
312	77.5	6.5	310	2	Q8D1I6	Q8D1I6 yersinia pe	385	77	6.4	3010	2	O9J3G4	O9J3G4 hepatitis c
313	77.5	6.5	310	2	AAS63427	AAS63427 yersinia	386	77	6.4	3013	2	Q6J6P5	Q6J6P5 hepatitis c
314	77.5	6.5	327	2	Q9POQ1	Q9POQ1 ureaplasma	387	77	6.4	4416	2	Q9J3F8	Q9J3F8 murine hepa
315	77.5	6.5	328	2	Q9K686	Q9K686 bacillus ha	388	77	6.4	4416	2	Q9J3F8	Q9J3F8 murine hepa
316	77.5	6.5	338	2	O42882	O42882 schizosacch	389	77	6.4	7124	1	R1AB_CVM2	R1AB_CVM2 replicase
317	77.5	6.5	365	2	Q8R770	Q8R770 thermococ	390	76.5	6.4	278	2	Q7ADZ1	Q7ADZ1 escherichia
318	77.5	6.5	379	2	O48008	O48008 perognathus	391	76.5	6.4	281	2	Q8XBF0	Q8XBF0 escherichia
319	77.5	6.5	392	2	Q8G7P7	Q8G7P7 bifidobacte	392	76.5	6.4	281	2	O8SKS9	O8SKS9 ancylostoma
320	77.5	6.5	411	2	O9P6N5	O9P6N5 schizosacch	393	76.5	6.4	282	2	Q92WV5	Q92WV5 rhizobium m
321	77.5	6.5	422	2	O9HKY6	O9HKY6 thermoplasm	394	76.5	6.4	342	2	Q7Z290	Q7Z290 caenorhabdi
322	77.5	6.5	440	2	Q9ZY23	Q9ZY23 pedinomonas	395	76.5	6.4	352	1	RNFD_SALT1	RNFD_SALT1 caenorhabdi
323	77.5	6.5	483	2	Q9G8V8	Q9G8V8 rhodomonas	396	76.5	6.4	352	1	RNFD_SALT2	RNFD_SALT2 salmonella

397	76.5	6.4	379	1	CYB DIPOR	Q9gaw3 dipodomys o	470	75.5	6.3	248	2	Q6HMF5	Q6hmf5 bacillus th
398	76.5	6.4	379	2	Q9G8Y7	Q9gbw7 ochotona pa	471	75.5	6.3	263	2	Q6HNS6	Q6hns6 bacillus th
399	76.5	6.4	380	2	Q8HNI7	Q8hni7 praomys nat	472	75.5	6.3	263	2	Q81YU8	Q81yu8 bacillus th
400	76.5	6.4	395	2	Q8KHK2	Q8khn2 pseudomonas	473	75.5	6.3	283	2	Q8CVF4	Q8cyf4 streptococc
401	76.5	6.4	415	2	Q7UBI3	Q7ub13 shigella fl	474	75.5	6.3	283	2	Q97FD2	Q97pd2 streptococc
402	76.5	6.4	415	2	Q83PL5	Q83pl5 shigella fl	475	75.5	6.3	283	2	Q865K7	Aat29627 bacillus
403	76.5	6.4	438	1	CLN3 MOUSE	Q83pl5 shigella fl	476	75.5	6.3	303	2	AAT29627	Q865k7 macropus eu
404	76.5	6.4	453	2	Q6ZGZ4	Q6zgz4 mus musculu	477	75.5	6.3	303	2	Q9KZ08	Q9kz08 streptomyc
405	76.5	6.4	453	2	BAD07667	Bad07667 oryza sat	478	75.5	6.3	310	2	Q870H5	Q870h5 saccharomyc
406	76.5	6.4	462	2	Q82V00	Q82v00 nitrosomona	479	75.5	6.3	326	2	Q9ESJ3	Q9esj3 rattus norv
407	76.5	6.4	468	1	IDBM CAEEL	Q82v00 nitrosomona	480	75.5	6.3	339	2	Q870H5	Q870h5 saccharomyc
408	76.5	6.4	490	2	Q6SX39	Q6sx39 human cyt	481	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
409	76.5	6.4	490	2	AAR31303	Aar31303 human cyt	482	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
410	76.5	6.4	491	2	AAR31303	Aar31303 human cyt	483	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
411	76.5	6.4	491	2	AAR31303	Aar31303 human cyt	484	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
412	76.5	6.4	500	2	Q96Z43	Q96z43 sulfolobus	485	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
413	76.5	6.4	526	1	FVR2 HUMAN	Q96z43 sulfolobus	486	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
414	76.5	6.4	526	2	Q96Z43	Q96z43 sulfolobus	487	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
415	76.5	6.4	528	2	Q96Z43	Q96z43 sulfolobus	488	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
416	76.5	6.4	538	2	Q96Z43	Q96z43 sulfolobus	489	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
417	76.5	6.4	555	2	Q96Z43	Q96z43 sulfolobus	490	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
418	76.5	6.4	570	2	Q96Z43	Q96z43 sulfolobus	491	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
419	76.5	6.4	589	2	Q96Z43	Q96z43 sulfolobus	492	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
420	76.5	6.4	614	2	Q96Z43	Q96z43 sulfolobus	493	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
421	76.5	6.4	627	2	Q96Z43	Q96z43 sulfolobus	494	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
422	76.5	6.4	687	2	Q96Z43	Q96z43 sulfolobus	495	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
423	76.5	6.4	743	2	Q96Z43	Q96z43 sulfolobus	496	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
424	76.5	6.4	839	2	Q96Z43	Q96z43 sulfolobus	497	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
425	76.5	6.4	909	2	Q96Z43	Q96z43 sulfolobus	498	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
426	76.5	6.4	1485	2	Q96Z43	Q96z43 sulfolobus	499	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
427	76.5	6.4	1641	2	Q96Z43	Q96z43 sulfolobus	500	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
428	76.5	6.4	156	2	Q96Z43	Q96z43 sulfolobus	501	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
429	76.5	6.4	201	2	Q96Z43	Q96z43 sulfolobus	502	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
430	76.5	6.4	210	2	Q96Z43	Q96z43 sulfolobus	503	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
431	76.5	6.4	255	2	Q96Z43	Q96z43 sulfolobus	504	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
432	76.5	6.4	255	2	Q96Z43	Q96z43 sulfolobus	505	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
433	76.5	6.4	272	2	Q96Z43	Q96z43 sulfolobus	506	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
434	76.5	6.4	292	2	Q96Z43	Q96z43 sulfolobus	507	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
435	76.5	6.4	325	2	Q96Z43	Q96z43 sulfolobus	508	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
436	76.5	6.4	342	1	NU2M LOCMI	Q96z43 sulfolobus	509	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
437	76.5	6.4	402	2	Q21933	Q21933 caenorhabdi	510	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
438	76.5	6.4	425	2	Q9URS2	Q91r82 actinobacil	511	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
439	76.5	6.4	425	2	Q9URS2	Q91r82 actinobacil	512	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
440	76.5	6.4	461	2	Q85002	Q85002 streptococc	513	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
441	76.5	6.4	461	2	Q85002	Q85002 streptococc	514	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
442	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	515	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
443	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	516	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
444	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	517	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
445	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	518	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
446	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	519	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
447	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	520	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
448	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	521	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
449	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	522	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
450	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	523	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
451	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	524	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
452	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	525	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
453	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	526	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
454	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	527	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
455	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	528	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
456	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	529	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
457	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	530	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
458	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	531	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
459	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	532	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
460	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	533	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
461	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	534	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
462	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	535	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
463	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	536	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
464	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	537	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
465	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	538	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
466	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	539	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
467	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	540	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
468	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	541	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe
469	76.5	6.4	474	2	Q72SX4	Q72sx4 leptospira	542	75.5	6.3	352	1	Q9QEV3	Q9qev3 human herpe

543	75	6.3	380	1	CYB_RANRU	Q8t6r3 rana rugosa	616	74.5	6.2	1808	2	Q9LYS6	Q9ly66 arabidopsis
544	75	6.3	387	2	Q46657	Q46657 sus scrofa	617	74.5	6.2	1837	2	Q8IKF1	Q8ikf1 plasmodium
545	75	6.3	407	2	QNRFS	Qnrfs cymbobacte	618	74.5	6.2	3010	2	Q91AU0	Q91au0 hepatitis c
546	75	6.3	418	2	Q6QFB8	Q6qfb8 legionella	619	74	6.2	124	2	Q8KC46	Q8kc46 chlorobium
547	75	6.3	418	2	RAS92188	Aas92188 legionell	620	74	6.2	156	2	Q81528	Q81528 hepatitis c
548	75	6.3	473	1	GAR1_HUMAN	P24046 homo sapien	621	74	6.2	167	2	Q8WZ72	Q8wz72 homo sapien
549	75	6.3	488	2	Q7RWF8	Q7rws8 neurospora	622	74	6.2	225	2	Q91SA2	Q91sa2 avian infec
550	75	6.3	498	2	Q75U67	Q75u67 fugu rubrip	623	74	6.2	230	2	Q88Y70	Q88y70 lactobacill
551	75	6.3	498	2	BAD02935	Bad02935 fugu rubr	624	74	6.2	231	1	CBS2_ARCFU	O27961 archaeoglob
552	75	6.3	526	2	Q9SN21	Q9sn21 arabidopsis	625	74	6.2	231	2	O28892	O28892 archaeoglob
553	75	6.3	543	2	Q7NS50	Q7ns50 cymbobacte	626	74	6.2	238	2	Q6HET1	Q6het1 bacillus th
554	75	6.3	649	2	O34952	O34952 bacillus su	627	74	6.2	255	2	Q66483	Q66483 equine arte
555	75	6.3	662	2	Q7VED4	Q7ved4 prochloroco	628	74	6.2	278	2	O6CUI8	O6cui8 kluyveromyc
556	75	6.3	753	2	Q98S90	Q98s90 guillardia	629	74	6.2	286	1	POTB_MYCPN	P5058 mycoplasma
557	75	6.3	777	2	Q6BG55	Q6bg55 parametium	630	74	6.2	294	2	Q9SM72	Q9sm72 oryza sativ
558	75	6.3	885	2	O8PUL6	Q8pul6 methanosarc	631	74	6.2	295	1	CYOE_PSEPU	Q9wvr5 pseudomonas
559	75	6.3	937	2	O82Z87	Q82z87 enterococcu	632	74	6.2	295	2	Q6S4M3	Q6s4m3 pseudomonas
560	75	6.3	1008	2	O89152	O89152 hepatitis c	633	74	6.2	295	2	AAS45860	Aas45860 pseudomon
561	75	6.3	1008	2	O89153	O89153 hepatitis c	634	74	6.2	300	1	NU2M_ASCSU	P24877 ascaris suu
562	75	6.3	1008	2	O89156	O89156 hepatitis c	635	74	6.2	312	1	PYRB_AERPE	Q9ybd4 aeropyrum p
563	75	6.3	1131	2	Q8NAT5	Q8nat5 homo sapien	636	74	6.2	312	2	Q9CH74	Q9ch74 lactococcus
564	75	6.3	1145	2	O8GUE7	Q8gue7 cymodocea n	637	74	6.2	315	2	Q710S2	Q710s2 spalax leuc
565	75	6.3	1154	2	O6FT16	O6ft16 candida gla	638	74	6.2	315	2	CAC95210	Cac95210 spalax le
566	75	6.3	1336	2	O6FLJ1	O6flj1 mesoplasma	639	74	6.2	321	2	Q8M6V0	Q8m6v0 tigrilopus j
567	75	6.3	1704	2	Q95206	Q95z06 trypanosoma	640	74	6.2	324	2	O8DVZ6	Q8dvz6 streptococc
568	75	6.3	2248	1	CYAL_DROME	P32870 drosophila	641	74	6.2	349	1	I10S_MOUSE	Q6i190 mus musculu
569	75	6.3	2248	1	Q9VY17	Q9vy17 drosophila	642	74	6.2	350	1	ML1A_HUMAN	P48039 homo sapien
570	75	6.3	3010	2	Q68833	Q68833 hepatitis c	643	74	6.2	351	2	Q8VHM7	Q8vhm7 mus musculu
571	75	6.3	3010	2	Q9J3G2	Q9j3g2 hepatitis c	644	74	6.2	379	1	CYB_THOMO	Q8wek2 thomomys mo
572	75	6.3	3010	2	Q9J3G5	Q9j3g5 hepatitis c	645	74	6.2	379	2	O47980	O47980 thomomys bo
573	75	6.3	3010	2	Q9Q1V7	Q9q1v7 hepatitis c	646	74	6.2	379	2	O48002	O48002 thomomys mo
574	75	6.3	3010	2	Q9Q1V8	Q9q1v8 hepatitis c	647	74	6.2	379	2	O48003	O48003 thomomys mo
575	74.5	6.2	174	2	P97068	P97068 salmonella	648	74	6.2	379	2	Q8HHJ7	Q8hhj7 thomomys bo
576	74.5	6.2	179	2	O8EPH9	Q8eph9 oceanobacil	649	74	6.2	379	2	Q8WEK5	Q8wek5 thomomys ta
577	74.5	6.2	180	2	P71253	P71253 escherichia	650	74	6.2	380	2	Q74KB0	Q74kb0 lactobacill
578	74.5	6.2	227	2	Q9GAT4	Q9gat4 ochotona cu	651	74	6.2	380	2	AAS08662	Aas08662 lactobaci
579	74.5	6.2	227	2	Q9GAT5	Q9gat5 ochotona th	652	74	6.2	381	1	CYB_PSENI	Q35533 pseudantech
580	74.5	6.2	227	2	Q9GAT6	Q9gat6 ochotona pr	653	74	6.2	396	2	O6GAR1	Q6gar1 staphylococ
581	74.5	6.2	258	2	Q88WC7	Q88wc7 lactobacill	654	74	6.2	396	2	O6GI68	Q6gi68 staphylococ
582	74.5	6.2	276	2	Q9R9G5	Q9r9g5 rhizobium m	655	74	6.2	396	2	Q8NXC4	Q8nxc4 staphylococ
583	74.5	6.2	280	2	O6WIF6	O6wif6 synecococc	656	74	6.2	396	2	Q99V76	Q99v76 staphylococ
584	74.5	6.2	280	2	AAQ23047	AAQ23047 synecococ	657	74	6.2	396	2	O7A6D3	O7a6d3 staphylococ
585	74.5	6.2	290	2	Q6SEU1	Q6seul uncultured	658	74	6.2	418	2	O6QFB9	Q6qfb9 legionella
586	74.5	6.2	290	2	AAR38481	Aar38481 unculture	659	74	6.2	418	2	Q6QFC5	Q6qfc5 legionella
587	74.5	6.2	298	2	Q6BWD3	Q6bwd3 debaryomyce	660	74	6.2	418	2	O6QFC7	Q6qfc7 legionella
588	74.5	6.2	313	2	Q8R7K6	Q8r7k6 thermoanaer	661	74	6.2	418	2	AAS92179	Aas92179 legionell
589	74.5	6.2	335	2	Q9WXS7	Q9wxs7 thermotoga	662	74	6.2	418	2	AAS92181	Aas92181 legionell
590	74.5	6.2	335	2	C3X1_HUMAN	P49238 homo sapien	663	74	6.2	418	2	AAS92187	Aas92187 legionell
591	74.5	6.2	364	2	Q8IDY2	Q8idy2 plasmodium	664	74	6.2	442	2	Q9CEG6	Q9ceg6 lactococcus
592	74.5	6.2	377	2	Q766W3	Q766w3 vargula hil	665	74	6.2	457	2	Q8RBZ7	Q8rbz7 thermoanaer
593	74.5	6.2	377	2	BAD06245	Bad06245 vargula h	666	74	6.2	475	2	Q9S2G7	Q9s2g7 streptomyce
594	74.5	6.2	378	2	Q6DUV8	Q6duv8 brassica na	667	74	6.2	485	2	Q9XVK0	Q9xvk0 caenorhabdi
595	74.5	6.2	379	1	CYB_OCHPR	Q9gbz4 ochotona pr	668	74	6.2	487	2	O23384	O23384 arabidopsis
596	74.5	6.2	379	2	Q9B9E3	Q9b9e3 chaetodipus	669	74	6.2	493	2	Q9EVJ7	Q9evj7 flavobacter
597	74.5	6.2	379	2	Q8WB05	Q8wb05 apicomontia	670	74	6.2	503	2	Q6M052	Q6m052 methanococc
598	74.5	6.2	392	2	Q9LCN4	Q9lcn4 micromonosp	671	74	6.2	503	2	CAF299975	CAF29975 methanoco
599	74.5	6.2	442	2	Q94A13	Q94a13 arabidopsis	672	74	6.2	528	2	Q701Q9	Q701q9 kluyveromyc
600	74.5	6.2	471	1	5H2A_RAT	P14842 rattus norv	673	74	6.2	528	2	CAF29008	CAF29008 kluyverom
601	74.5	6.2	473	2	Q9K5Y9	Q9k5y9 bacillus ha	674	74	6.2	540	2	O6LF33	O6lf33 plasmodium
602	74.5	6.2	488	2	Q6QU71	Q6qu71 aspergillus	675	74	6.2	540	2	CAG24999	Cag24999 plasmodiu
603	74.5	6.2	488	2	AAS66783	Aas66783 aspergill	676	74	6.2	581	2	O6FI16	O6fi16 candida gla
604	74.5	6.2	500	2	O24348	O24348 sorghum bic	677	74	6.2	650	2	Q9S6S6	Q9s6s6 lactococcus
605	74.5	6.2	562	2	Q8N2S3	Q8n2s3 homo sapien	678	74	6.2	742	2	O6FNV6	O6fnv6 candida gla
606	74.5	6.2	574	2	O22454	O22454 triticum ae	679	74	6.2	841	2	Q9AIP1	Q9aip1 carsonella
607	74.5	6.2	597	2	Q9VD40	Q9vd40 drosophila	680	74	6.2	846	2	Q93U47	Q93u47 carsonella
608	74.5	6.2	618	1	YKR4_YEAST	P36029 saccharomyc	681	74	6.2	892	2	O8TGB2	O8tgb2 candida alb
609	74.5	6.2	848	2	Q8VVK9	Q8vvk9 corynebacte	682	74	6.2	1123	2	Q9SE99	Q9ses9 arabidopsis
610	74.5	6.2	990	1	FTSK_VIBVU	Q8d8m2 vibrio vuln	683	74	6.2	1123	2	Q9SEU7	Q9sep7 arabidopsis
611	74.5	6.2	1033	2	Q7Z2C1	Q7z2c1 trypanosoma	684	74	6.2	3010	2	Q9J3H6	Q9j3h6 hepatitis c
612	74.5	6.2	1034	2	Q7Z2C0	Q7z2c0 trypanosoma	685	74	6.2	3010	2	Q9Q1V1	Q9q1v1 hepatitis c
613	74.5	6.2	1183	2	Q94447	Q94447 caliphora	686	74	6.2	3010	2	Q9Q1Y2	Q9qi2 hepatitis c
614	74.5	6.2	1520	2	Q8T687	Q8t687 dictyosteli	687	74	6.2	3010	2	Q9DTE8	Q9dte8 hepatitis c
615	74.5	6.2	1559	2	Q780S1	Q780s1 neurospora	688	74	6.2	3010	2	Q9J3V3	Q9j3v3 hepatitis c

689	73.5	6.2	120	2	Q9SKA6	Q9SKA6 arabidopsis	762	73	6.1	156	2	Q81510	Q81510 hepatitis c
690	73.5	6.2	153	2	Q92XD3	Q92XD3 rhizobium m	763	73	6.1	156	2	Q81522	Q81522 hepatitis c
691	73.5	6.2	180	2	Q8ZXS3	Q8ZXS3 pyrobaculum	764	73	6.1	156	2	Q81537	Q81537 hepatitis c
692	73.5	6.2	180	2	P71251	P71251 escherichia	765	73	6.1	163	2	Q80RY8	Q80RY8 avian infec
693	73.5	6.2	180	2	P71257	P71257 escherichia	766	73	6.1	220	2	Q72Z40	Q72Z40 bacillus ce
694	73.5	6.2	180	2	P75018	P75018 escherichia	767	73	6.1	220	2	AA543730	AA543730 bacillus
695	73.5	6.2	199	2	Q8DVR3	Q8DVR3 streptococ	768	73	6.1	223	1	VNEI_IBVG	VNEI_IBVG avian infec
696	73.5	6.2	216	1	YK36_AQUAE	YK36_AQUAE aquifex aeo	769	73	6.1	223	1	Q91S97	Q91S97 avian infec
697	73.5	6.2	226	2	Q9J0X1	Q9J0X1 avian infec	770	73	6.1	226	2	Q7T9P6	Q7T9P6 avian infec
698	73.5	6.2	270	2	Q8HBP0	Q8HBP0 perognathus	771	73	6.1	238	1	PYRF_BACCR	PYRF_BACCR avian infec
699	73.5	6.2	270	2	Q8HBP6	Q8HBP6 perognathus	772	73	6.1	238	2	Q732T6	Q732T6 bacillus ce
700	73.5	6.2	274	2	Q95L51	Q95L51 capra hircu	773	73	6.1	238	2	AA542831	AA542831 bacillus
701	73.5	6.2	288	2	Q6Z2T3	Q6Z2T3 oryza sativ	774	73	6.1	249	2	Q9FDU6	Q9FDU6 streptococ
702	73.5	6.2	298	2	BAD15544	BAD15544 oryza sat	775	73	6.1	255	2	P87639	P87639 equine arte
703	73.5	6.2	318	2	BAD16128	BAD16128 oryza sat	776	73	6.1	255	2	Q9YNU0	Q9YNU0 equine arte
704	73.5	6.2	318	2	Q55895	Q55895 synchocyst	777	73	6.1	261	2	Q7QN39	Q7QN39 anopheles g
705	73.5	6.2	338	1	YYAD_BACSU	YYAD_BACSU bacillidiano	778	73	6.1	264	2	Q7MJ52	Q7MJ52 vibrio vuln
706	73.5	6.2	360	2	Q8UUV8	Q8UUV8 brachydanio	779	73	6.1	264	2	Q8DAQ9	Q8DAQ9 vibrio vuln
707	73.5	6.2	379	1	CYB_PHOGR	CYB_PHOGR thomomys ta	780	73	6.1	279	2	Q6TY95	Q6TY95 xiphinema a
708	73.5	6.2	379	1	CYB_THOTA	CYB_THOTA ochotona cu	781	73	6.1	279	2	AAQ75777	AAQ75777 xiphinema
709	73.5	6.2	380	1	CYB_STRPU	CYB_STRPU strongyloce	782	73	6.1	282	1	NU2M_CAEEL	NU2M_CAEEL caenorhabdi
710	73.5	6.2	380	1	OPGC_SALTI	OPGC_SALTI salmonella	783	73	6.1	290	2	Q6G9W4	Q6G9W4 staphylococ
711	73.5	6.2	384	1	OPGC_SALTY	OPGC_SALTY salmonella	784	73	6.1	290	2	Q8NX00	Q8NX00 staphylococ
712	73.5	6.2	384	1	OPGC_SALTY	OPGC_SALTY salmonella	785	73	6.1	295	2	Q8VUQ2	Q8VUQ2 pseudomonas
713	73.5	6.2	385	2	P94432	P94432 bacillus su	786	73	6.1	295	2	Q88PN3	Q88PN3 pseudomonas
714	73.5	6.2	387	2	Q9KMU2	Q9KMU2 sphingomonas	787	73	6.1	303	2	Q94EJ0	Q94EJ0 arabidopsis
715	73.5	6.2	387	2	Q9KMU2	Q9KMU2 sphingomonas	788	73	6.1	314	2	Q8ESH3	Q8ESH3 oceanobacil
716	73.5	6.2	387	2	Q9KMU2	Q9KMU2 sphingomonas	789	73	6.1	326	2	Q9H6T9	Q9H6T9 homo sapien
717	73.5	6.2	391	1	Q9KMU2	Q9KMU2 sphingomonas	790	73	6.1	326	2	Q99NR7	Q99NR7 muscardinus
718	73.5	6.2	391	1	Q9KMU2	Q9KMU2 sphingomonas	791	73	6.1	335	1	Q8SML8	Q8SML8 encephalito
719	73.5	6.2	409	2	Q8Z2F7	Q8Z2F7 enterococcu	792	73	6.1	339	2	Q9N2T2	Q9N2T2 caenorhabdi
720	73.5	6.2	413	2	Q8Z2F7	Q8Z2F7 enterococcu	793	73	6.1	343	2	Q85AS7	Q85AS7 myrmica sul
721	73.5	6.2	421	2	Q8PK37	Q8PK37 xanthomonas	794	73	6.1	343	2	Q85AS7	Q85AS7 myrmica sul
722	73.5	6.2	421	2	Q8PK37	Q8PK37 xanthomonas	795	73	6.1	348	1	GHSR_MOUSE	GHSR_MOUSE mus musculu
723	73.5	6.2	425	2	Q8D6K1	Q8D6K1 erwinia car	796	73	6.1	364	1	GHSR_MOUSE	GHSR_MOUSE mus musculu
724	73.5	6.2	442	2	Q8GZ34	Q8GZ34 arabidopsis	797	73	6.1	364	1	GHSR_MOUSE	GHSR_MOUSE mus musculu
725	73.5	6.2	442	2	Q8GZ34	Q8GZ34 arabidopsis	798	73	6.1	364	1	GHSR_MOUSE	GHSR_MOUSE mus musculu
726	73.5	6.2	442	2	Q8GZ34	Q8GZ34 arabidopsis	799	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
727	73.5	6.2	491	2	Q7M6S4	Q7M6S4 human cyt	800	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
728	73.5	6.2	491	2	Q7M6S4	Q7M6S4 human cyt	801	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
729	73.5	6.2	518	2	Q8VZ22	Q8VZ22 arabidopsis	802	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
730	73.5	6.2	574	2	Q93P90	Q93P90 candida alb	803	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
731	73.5	6.2	574	2	Q93P90	Q93P90 candida alb	804	73	6.1	378	2	Q70EG4	Q70EG4 saccostomus
732	73.5	6.2	607	2	Q6DFJ5	Q6DFJ5 xenopus lae	805	73	6.1	379	2	Q34099	Q34099 cratogeomys
733	73.5	6.2	634	2	Q9PC78	Q9PC78 xylella fas	806	73	6.1	379	2	Q34099	Q34099 cratogeomys
734	73.5	6.2	637	1	MUTL_BACHD	MUTL_BACHD bacillus ha	807	73	6.1	379	2	Q34099	Q34099 cratogeomys
735	73.5	6.2	640	1	APRN_ENTHI	APRN_ENTHI entameba h	808	73	6.1	383	2	Q8GLD2	Q8GLD2 cynopterus
736	73.5	6.2	653	2	Q8TTH1	Q8TTH1 methanobac	809	73	6.1	391	1	Y450_BUCAP	Y450_BUCAP buchnera ap
737	73.5	6.2	661	2	Q8A468	Q8A468 corynebacte	810	73	6.1	394	2	Q6EE99	Q6EE99 latimeria c
738	73.5	6.2	731	2	Q16531	Q16531 caenorhabdi	811	73	6.1	399	2	Q6LQJ3	Q6LQJ3 picophilus
739	73.5	6.2	846	2	Q93U53	Q93U53 carsonella	812	73	6.1	401	2	Q6KXZ3	Q6KXZ3 picophilus
740	73.5	6.2	1049	2	Q8FTY2	Q8FTY2 candida gla	813	73	6.1	446	2	Q8H9B3	Q8H9B3 brassica ca
741	73.5	6.2	1095	2	Q9C7H5	Q9C7H5 arabidopsis	814	73	6.1	450	1	VGLM_EHV1B	VGLM_EHV1B equine herp
742	73.5	6.2	1174	2	Q7M006	Q7M006 murine hepa	815	73	6.1	450	2	Q6S6V2	Q6S6V2 equine herp
743	73.5	6.2	1277	2	Q7M006	Q7M006 murine hepa	816	73	6.1	450	2	Q6S6V2	Q6S6V2 equine herp
744	73.5	6.2	1277	2	Q7M006	Q7M006 murine hepa	817	73	6.1	450	2	Q6S6V2	Q6S6V2 equine herp
745	73.5	6.2	1287	2	Q7YU59	Q7YU59 drosophila	818	73	6.1	453	2	Q94307	Q94307 caenorhabdi
746	73.5	6.2	1287	2	Q7YU59	Q7YU59 drosophila	819	73	6.1	453	2	Q94307	Q94307 caenorhabdi
747	73.5	6.2	1287	2	Q7YU59	Q7YU59 drosophila	820	73	6.1	453	2	Q94307	Q94307 caenorhabdi
748	73.5	6.2	1287	2	Q7YU59	Q7YU59 drosophila	821	73	6.1	453	2	Q94307	Q94307 caenorhabdi
749	73.5	6.2	1476	2	Q965D3	Q965D3 drosophila	822	73	6.1	453	2	Q94307	Q94307 caenorhabdi
750	73.5	6.2	1545	2	Q8GU65	Q8GU65 oryza sativ	823	73	6.1	453	2	Q94307	Q94307 caenorhabdi
751	73.5	6.2	2666	2	Q6FW99	Q6FW99 candida gla	824	73	6.1	453	2	Q94307	Q94307 caenorhabdi
752	73.5	6.2	3010	2	Q9DTE6	Q9DTE6 hepatitis c	825	73	6.1	453	2	Q94307	Q94307 caenorhabdi
753	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	826	73	6.1	453	2	Q94307	Q94307 caenorhabdi
754	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	827	73	6.1	453	2	Q94307	Q94307 caenorhabdi
755	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	828	73	6.1	453	2	Q94307	Q94307 caenorhabdi
756	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	829	73	6.1	453	2	Q94307	Q94307 caenorhabdi
757	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	830	73	6.1	453	2	Q94307	Q94307 caenorhabdi
758	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	831	73	6.1	453	2	Q94307	Q94307 caenorhabdi
759	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	832	73	6.1	453	2	Q94307	Q94307 caenorhabdi
760	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	833	73	6.1	453	2	Q94307	Q94307 caenorhabdi
761	73.5	6.2	3381	2	Q8IDK4	Q8IDK4 plasmodium	834	73	6.1	453	2	Q94307	Q94307 caenorhabdi

835	73	6.1	966	1	PKD2 MOUSE	Q15245 mus musculus	908	72.5	6.1	379	2	Q85AV3	Q85av3 chimarrogal
836	73	6.1	966	2	Q7TSI7	Q7tsi7 mus musculus	909	72.5	6.1	379	2	Q8G1C3	Q8g1c3 ochotona ca
837	73	6.1	966	2	Q8BPR6	Q8bpr6 mus musculus	910	72.5	6.1	379	2	Q9G1C4	Q9g1c4 ochotona an
838	73	6.1	966	2	AAH62969	Aah62969 mus muscu	911	72.5	6.1	379	2	Q9GAW7	Q9gaw7 chaetodipus
839	73	6.1	971	2	Q60337	Q60337 homo sapien	912	72.5	6.1	379	2	Q9GBY2	Q9gby2 ochotona ca
840	73	6.1	1035	2	Q967W1	Q967w1 schistosoma	913	72.5	6.1	379	2	Q9GBY8	Q9gby8 ochotona hu
841	73	6.1	1075	2	Q9LPE2	Q9lpe2 arabidopsis	914	72.5	6.1	379	2	Q9GBY9	Q9gby9 ochotona hy
842	73	6.1	1111	2	Q86FP2	Q86fp2 caenorhabdi	915	72.5	6.1	379	2	Q9GBZ1	Q9gbz1 ochotona la
843	73	6.1	1127	2	Q9N323	Q9n323 caenorhabdi	916	72.5	6.1	379	2	Q9GBZ3	Q9gbz3 ochotona pa
844	73	6.1	1931	2	Q8RJY3	Q8rjy3 stigmatella	917	72.5	6.1	379	2	Q8EWI6	Q8ewi6 mycoplasma
845	73	6.1	2010	2	Q7PZN7	Q7pzn7 anopheles g	918	72.5	6.1	379	2	CAD60959	Cad60959 ochotona
846	73	6.1	3010	2	P88803	P88803 hepatitis c	919	72.5	6.1	387	2	Q6RKP6	Q6rkp6 human herpe
847	73	6.1	3010	2	Q9J3G1	Q9j3g1 hepatitis c	920	72.5	6.1	387	2	AAT01423	Aat01423 human her
848	73	6.1	3010	2	Q9J3J0	Q9j3j0 hepatitis c	921	72.5	6.1	389	1	OXYP_HUMAN	P30559 homo sapien
849	73	6.1	3013	2	Q9QIX9	Q9qix9 hepatitis c	922	72.5	6.1	402	2	Q8WMQ9	Q8wmq9 ovis aries
850	73	6.1	3013	2	Q9QIY0	Q9qiyo hepatitis c	923	72.5	6.1	428	2	AAS2G86	Aas2g86 yersinia pe
851	73	6.1	6875	2	Q287Y3	Q287y3 cryptotlagus	924	72.5	6.1	428	2	AAS61416	Aas61416 yersinia
852	72.5	6.1	156	2	Q8L516	Q8l516 hepatitis c	925	72.5	6.1	442	2	Q6LOY3	Q6loy3 picrophilus
853	72.5	6.1	156	2	Q8L519	Q8l519 hepatitis c	926	72.5	6.1	442	2	Q6PHK5	Q6phk5 brachydanio
854	72.5	6.1	173	2	Q9WD17	Q9wd17 equine arte	927	72.5	6.1	442	2	AAH56518	Aah56518 brachydan
855	72.5	6.1	174	2	P97065	P97065 salmonella	928	72.5	6.1	445	2	Q6NYH8	Q6nyh8 brachydanio
856	72.5	6.1	180	2	P71252	P71252 escherichia	929	72.5	6.1	445	2	AAH66587	Aah66587 brachydan
857	72.5	6.1	180	2	P71254	P71254 escherichia	930	72.5	6.1	452	2	Q9T9N6	Q9t9n6 terebratuli
858	72.5	6.1	180	2	P71254	P71254 escherichia	931	72.5	6.1	457	2	Q6P822	Q6p822 xenopus tro
859	72.5	6.1	180	2	P71256	P71256 escherichia	932	72.5	6.1	457	2	AAH61409	Aah61409 xenopus t
860	72.5	6.1	180	2	P71258	P71258 escherichia	933	72.5	6.1	478	2	Q970D2	Q970d2 sulfobolus
861	72.5	6.1	180	2	P71259	P71259 escherichia	934	72.5	6.1	491	2	Q6SWL8	Q6swl8 human cytom
862	72.5	6.1	180	2	P71260	P71260 escherichia	935	72.5	6.1	491	2	AAR31477	Aar31477 human cyt
863	72.5	6.1	180	2	P71261	P71261 escherichia	936	72.5	6.1	499	1	MVIN_AQUAE	Q67658 aquifex aeo
864	72.5	6.1	191	2	Q8U4P0	Q8u4p0 pyrococcus	937	72.5	6.1	505	2	Q8QRV6	Q8qrv6 chimpanzee
865	72.5	6.1	208	2	Q63447	Q63447 echinotrix	938	72.5	6.1	513	1	PACR_BOVIN	Q29627 bos taurus
866	72.5	6.1	208	2	Q7J7L2	Q7j7l2 echinotrix	939	72.5	6.1	522	2	Q23444	Q23444 caenorhabdi
867	72.5	6.1	209	2	Q7J7L0	Q7j7l0 echinotrix	940	72.5	6.1	526	2	Q6PDF6	Q6pdf6 acinetobact
868	72.5	6.1	209	2	Q8GZ10	Q8gz10 arabidopsis	941	72.5	6.1	539	2	Q7VSL1	Q7vsl1 bordetella
869	72.5	6.1	209	2	Q49834	Q49834 mycobacteri	942	72.5	6.1	539	2	Q7W446	Q7w446 bordetella
870	72.5	6.1	210	2	Q7J7L9	Q7j7l9 echinotrix	943	72.5	6.1	539	2	Q7WFK3	Q7wfk3 bordetella
871	72.5	6.1	211	2	Q7J7L3	Q7j7l3 echinotrix	944	72.5	6.1	574	2	Q6LH28	Q6lh28 photobacter
872	72.5	6.1	214	2	Q63950	Q63950 echinotrix	945	72.5	6.1	574	2	CAG23402	Cag23402 photobact
873	72.5	6.1	217	2	Q9XMK7	Q9xmk7 ochotona pr	946	72.5	6.1	614	2	Q7U5J3	Q7u5j3 synecococc
874	72.5	6.1	224	2	Q8RGE6	Q8rge6 fusobacteri	947	72.5	6.1	635	2	Q21335	Q21335 caenorhabdi
875	72.5	6.1	255	2	Q7M2C0	Q7m2c0 leishmania	948	72.5	6.1	660	2	Q8AW53	Q8aw53 brachydanio
876	72.5	6.1	269	2	Q8RES9	Q8res9 fusobacteri	949	72.5	6.1	661	2	Q6G493	Q6g493 brachydanio
877	72.5	6.1	285	2	Q86DD6	Q86dd6 caenorhabdi	950	72.5	6.1	662	2	Q6G146	Q6g146 bartonella
878	72.5	6.1	291	2	Q24561	Q24561 zea mays (m	951	72.5	6.1	666	2	Q8E575	Q8e575 streptococc
879	72.5	6.1	298	2	Q8R2A8	Q8r2a8 mus musculu	952	72.5	6.1	671	2	Q6MCR0	Q6mcr0 parachlamy
880	72.5	6.1	308	2	Q6N472	Q6n472 rhodospseudo	953	72.5	6.1	671	2	CAP23639	Cap23639 parachlam
881	72.5	6.1	308	2	CAE28909	Caе28909 rhodopseu	954	72.5	6.1	688	2	Q8EKS6	Q8ekс6 shewanella
882	72.5	6.1	309	2	Q7LUE1	Q7lue1 bos taurus	955	72.5	6.1	696	2	Q9TU72	Q9tu72 mustela vis
883	72.5	6.1	309	2	AAC59889	Aac59889 bos tauru	956	72.5	6.1	717	2	Q7R1C0	Q7riс0 plasmodium
884	72.5	6.1	315	2	Q9LGG02	Q9lgg02 arabidopsis	957	72.5	6.1	718	2	Q48872	Q48872 lactobacill
885	72.5	6.1	320	1	QXA2_LACIA	Q9chz9 lactococcus	958	72.5	6.1	734	2	Q6ZPF2	Q6zpf2 mus musculu
886	72.5	6.1	325	2	Q9CII9	Q9cii9 lactococcus	959	72.5	6.1	734	2	BAC98285	Bac98285 mus muscu
887	72.5	6.1	336	2	Q17077	Q17077 caenorhabdi	960	72.5	6.1	756	2	Q8C9E3	Q8c9e3 mus musculu
888	72.5	6.1	348	2	Q9924	Q9924 cyprinella	961	72.5	6.1	769	2	Q9N3Y9	Q9n3y9 caenorhabdi
889	72.5	6.1	348	2	Q833B9	Q833b9 enterococcu	962	72.5	6.1	848	2	Q9SIU2	Q9siu2 arabidopsis
890	72.5	6.1	350	2	Q835L2	Q835l2 enterococcu	963	72.5	6.1	848	2	Q8VZH3	Q8vzh3 arabidopsis
891	72.5	6.1	356	2	Q8FXM4	Q8fxm4 bruceella su	964	72.5	6.1	858	2	Q74IE5	Q74ies lactobacill
892	72.5	6.1	360	2	Q70US3	Q70us3 dirofilaria	965	72.5	6.1	858	2	AAS03933	Aas03933 lactobaci
893	72.5	6.1	360	2	CAD61193	Cad61193 dirofilar	966	72.5	6.1	1103	2	AAS03933	Aas03933 lactobaci
894	72.5	6.1	363	2	Q6HGU9	Q6hgu9 bacillus th	967	72.5	6.1	1103	2	AAS53655	Aas53655 ashbya go
895	72.5	6.1	374	2	Q8WMK0	Q8wmr0 ovis aries	968	72.5	6.1	1304	2	Q8MNU0	Q8mnj0 dictyosteli
896	72.5	6.1	379	1	CYB_OCHAL	Q9gby1 ochotona al	969	72.5	6.1	1357	2	Q8I7K7	Q8i7k7 caenorhabdi
897	72.5	6.1	379	1	CYB_OCHCU	Q9g1b9 ochotona cy	970	72.5	6.1	1526	2	Q19611	Q19611 caenorhabdi
898	72.5	6.1	379	1	CYB_OCHHI	Q9gby6 ochotona hi	971	72.5	6.1	1548	2	Q7Q409	Q7q409 anopheles g
899	72.5	6.1	379	1	CYB_OCHHY	Q9g62 ochotona hy	972	72.5	6.1	1689	2	Q991H9	Q991h9 cramean-con
900	72.5	6.1	379	1	CYB_OCHKO	Q9gbz0 ochotona ko	973	72.5	6.1	1689	2	Q8QZF4	Q8qzf4 crimean-con
901	72.5	6.1	379	1	CYB_OCHNB	Q9gbz2 ochotona nu	974	72.5	6.1	1702	2	Q95QK2	Q95qk2 caenorhabdi
902	72.5	6.1	379	1	CYB_OCHRO	Q9gbz5 ochotona ro	975	72.5	6.1	4037	2	Q7RG07	Q7rg07 plasmodium
903	72.5	6.1	379	1	CYB_OCHTH	Q9zzul ochotona th	976	72.5	6.1	114	2	Q6VRK9	Q6vrk9 helicobacte
904	72.5	6.1	379	1	CYB_OCHTU	Q9gbz6 ochotona th	977	72.5	6.0	114	2	AAR03928	Aar03928 helicobac
905	72.5	6.1	379	1	CYB_OCHTI	Q9gbz7 ochotona th	978	72.5	6.0	156	2	Q81540	Q81540 hepatitis c
906	72.5	6.1	379	2	Q70UT5	Q70ut5 ochotona pr	979	72.5	6.0	173	2	Q9WD22	Q9wd22 equine arte
907	72.5	6.1	379	2	Q71LX8	Q71lx8 ochotona ca	980	72.5	6.0	173	2	Q9WD25	Q9wd25 equine arte

981	72	6.0	182	2	Q98815	Q98815 rhizobium 1	1054	72	6.0	556	2	Q93YN6	Q93YN6 arabidopsis
982	72	6.0	200	2	Q41199	Q41199 porcine rep	1055	72	6.0	562	2	Q6CF79	Q6CF79 yarrowia li
983	72	6.0	200	2	Q9J7J6	Q9J7J6 porcine rep	1056	72	6.0	594	2	Q7L8K9	Q7L8K9 homo sapien
984	72	6.0	209	2	Q85U10	Q85U10 ciona savig	1057	72	6.0	596	2	Q8R7C9	Q8R7C9 thermoac
985	72	6.0	225	2	Q6DTU8	Q6DTU8 avian infec	1058	72	6.0	600	2	Q42972	Q42972 schizosacch
986	72	6.0	226	2	Q7TEH2	Q7TEH2 avian infec	1059	72	6.0	610	2	Q84ZX2	Q84ZX2 tetraselmis
987	72	6.0	227	2	Q7Y6X7	Q7Y6X7 tigrionus c	1060	72	6.0	630	2	Q24608	Q24608 dianthus ca
988	72	6.0	229	2	Q20551	Q20551 ursus ameri	1061	72	6.0	692	2	Q6DD44	Q6DD44 xenopus lae
989	72	6.0	249	2	Q8E9R2	Q8E9R2 shewanella	1063	72	6.0	696	2	Q9UBH6	Q9UBH6 homo sapien
990	72	6.0	254	2	Q81M08	Q81M08 bacillus ce	1064	72	6.0	712	2	Q94EK6	Q94EK6 pisum sativ
991	72	6.0	254	2	Q81M08	Q81M08 bacillus ce	1064	72	6.0	696	2	Q9UBH6	Q9UBH6 homo sapien
992	72	6.0	254	2	AAT33364	AAT33364 bacillus	1065	72	6.0	712	2	Q94EK6	Q94EK6 pisum sativ
993	72	6.0	276	2	Q9HJV7	Q9HJV7 thermoplas	1066	72	6.0	736	2	Q7YU76	Q7YU76 photorhabd
994	72	6.0	279	2	Q9XKT1	Q9XKT1 caenorhabdi	1067	72	6.0	772	2	Q7YU76	Q7YU76 drosophila
995	72	6.0	286	2	Q6HK77	Q6HK77 bacillus th	1068	72	6.0	772	2	Q7YU76	Q7YU76 drosophila
996	72	6.0	290	2	Q6SHA6	Q6SHA6 uncultured	1069	72	6.0	772	2	Q7YU76	Q7YU76 drosophila
997	72	6.0	290	2	AAR37714	AAR37714 uncultured	1070	72	6.0	788	2	Q7YU76	Q7YU76 drosophila
998	72	6.0	306	2	Q6HWV3	Q6HWV3 bacillus an	1071	72	6.0	796	2	Q7YU76	Q7YU76 drosophila
999	72	6.0	306	2	Q8Y980	Q8Y980 listeria mo	1072	72	6.0	796	2	Q7YU76	Q7YU76 drosophila
1000	72	6.0	306	2	Q6QDA2	Q6QDA2 lepisosteus	1073	72	6.0	844	2	Q7YU76	Q7YU76 drosophila
1001	72	6.0	306	2	AAS49414	AAS49414 lepisoste	1074	72	6.0	844	2	Q7YU76	Q7YU76 drosophila
1002	72	6.0	311	2	Q8VF62	Q8VF62 mus musculu	1075	72	6.0	878	2	Q7YU76	Q7YU76 drosophila
1003	72	6.0	317	2	Q9CKI6	Q9CKI6 pasteurella	1076	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1004	72	6.0	320	2	Q7ZUC3	Q7ZUC3 brachydanio	1077	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1005	72	6.0	323	2	Q88TJ9	Q88TJ9 lactobacill	1078	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1006	72	6.0	334	2	Q88X19	Q88X19 lactobacill	1079	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1007	72	6.0	335	2	Q9ZV32	Q9ZV32 orycteropus	1080	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1008	72	6.0	338	2	Q9XTR2	Q9XTR2 caenorhabdi	1081	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1009	72	6.0	339	2	Q97GD6	Q97GD6 clostridium	1082	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1010	72	6.0	343	2	Q85AT6	Q85AT6 uma scopari	1083	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1011	72	6.0	343	2	Q9TD07	Q9TD07 rachovia ma	1084	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1012	72	6.0	343	2	Q9B4H5	Q9B4H5 uma scopari	1085	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1013	72	6.0	343	2	Q9B4H5	Q9B4H5 uma scopari	1086	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1014	72	6.0	379	1	Q9B4H5	Q9B4H5 uma scopari	1087	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1015	72	6.0	379	1	Q9B4H5	Q9B4H5 uma scopari	1088	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1016	72	6.0	379	2	Q7IIQ9	Q7IIQ9 cratogeomys	1089	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1017	72	6.0	379	2	Q9THD6	Q9THD6 orycteropus	1090	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1018	72	6.0	379	2	Q8W8K4	Q8W8K4 cratogeomys	1091	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1019	72	6.0	379	2	Q8W8K4	Q8W8K4 cratogeomys	1092	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1020	72	6.0	386	1	Q9B4H5	Q9B4H5 uma scopari	1093	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1021	72	6.0	391	2	Q8RLX7	Q8RLX7 salmonella	1094	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1022	72	6.0	391	2	Q8RLX7	Q8RLX7 salmonella	1095	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1023	72	6.0	392	2	Q9LCN9	Q9LCN9 micromonospor	1096	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1024	72	6.0	396	1	Q9B4H5	Q9B4H5 uma scopari	1097	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1025	72	6.0	415	1	L52_ADE02	L52_ADE02 human ade	1098	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1026	72	6.0	415	1	L52_ADE05	L52_ADE05 human ade	1099	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1027	72	6.0	415	1	Q6VGW2	Q6VGW2 human ade	1100	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1028	72	6.0	415	2	Q7L1B5	Q7L1B5 human ade	1101	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1029	72	6.0	415	2	Q7M522	Q7M522 human ade	1102	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1030	72	6.0	415	2	Q7M522	Q7M522 human ade	1103	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1031	72	6.0	415	2	Q7M522	Q7M522 human ade	1104	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1032	72	6.0	415	2	Q7M522	Q7M522 human ade	1105	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1033	72	6.0	417	2	Q9NT19	Q9NT19 homo sapien	1106	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1034	72	6.0	418	2	Q6QFC3	Q6QFC3 legionella	1107	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1035	72	6.0	418	2	Q6QFC3	Q6QFC3 legionella	1108	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1036	72	6.0	418	2	Q6QFC3	Q6QFC3 legionella	1109	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1037	72	6.0	418	2	Q6QFC3	Q6QFC3 legionella	1110	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1038	72	6.0	444	2	Q6GKS5	Q6GKS5 staphylococ	1111	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1039	72	6.0	448	1	Q6GKS5	Q6GKS5 staphylococ	1112	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1040	72	6.0	448	1	Q6GKS5	Q6GKS5 staphylococ	1113	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1041	72	6.0	448	1	Q6GKS5	Q6GKS5 staphylococ	1114	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1042	72	6.0	453	2	Q99XF2	Q99XF2 staphylococ	1115	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1043	72	6.0	453	2	Q99XF2	Q99XF2 staphylococ	1116	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1044	72	6.0	465	2	Q99XF2	Q99XF2 staphylococ	1117	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1045	72	6.0	468	2	Q99XF2	Q99XF2 staphylococ	1118	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1046	72	6.0	479	1	Q99XF2	Q99XF2 staphylococ	1119	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1047	72	6.0	497	1	Q99XF2	Q99XF2 staphylococ	1120	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1048	72	6.0	518	2	Q7VQX6	Q7VQX6 candidatus	1121	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1049	72	6.0	523	2	Q86YB4	Q86YB4 homo sapien	1122	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1050	72	6.0	530	2	Q65124	Q65124 african ewi	1123	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1051	72	6.0	552	2	Q6NHU7	Q6NHU7 corynebacte	1124	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1052	72	6.0	552	2	Q6NHU7	Q6NHU7 corynebacte	1125	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila
1053	72	6.0	553	2	Q975L9	Q975L9 sulfolobus	1126	72	6.0	1035	2	Q7YU76	Q7YU76 drosophila

1127	71.5	6.0	342	2	AAC34949	Aac34949 kaposi's	1200	71.5	6.0	858	2	Q861Y5	O861y5 dictyosteli
1128	71.5	6.0	342	2	AAK33416	Aak33416 kaposi's	1201	71.5	6.0	890	1	WFS1_HUMAN	Q76024 homo sapien
1129	71.5	6.0	342	2	AAK33418	Aak33418 kaposi's	1202	71.5	6.0	1407	1	CYAA_HUMAN	Q03100 dictyosteli
1130	71.5	6.0	342	2	AAK33419	Aak33419 kaposi's	1203	71.5	6.0	1509	2	AAR89623	Q6rcs2 ciona savig
1131	71.5	6.0	345	2	Q9T200	Q9t200 caenorhabdi	1204	71.5	6.0	1509	2	AAR89623	Aar89623 ciona sav
1132	71.5	6.0	348	1	RNFD_VTBCH	Q9kt89 vibrio chol	1205	71.5	6.0	2837	2	Q6X3J2	Q6x3j2 pseudomonas
1133	71.5	6.0	348	2	Q99322	Q99322 cyprinella	1206	71.5	6.0	2837	2	Q6X3J2	Q6x3j2 pseudomonas
1134	71.5	6.0	355	2	Q8YDX2	Q8ydx2 bruceella me	1207	71.5	6.0	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
1135	71.5	6.0	360	2	Q8HIB6	Q8hib6 callosiclu	1208	71.5	6.0	3010	2	Q68949	Q68949 hepatitis c
1136	71.5	6.0	362	2	Q6PDF2	Q6pdf2 mus musculu	1209	71.5	6.0	3589	2	Q6LF63	Q6lf63 plasmodium
1137	71.5	6.0	362	2	AAH58742	Aah58742 mus muscu	1210	71.5	6.0	3589	2	CAG25008	Cag25008 plasmodiu
1138	71.5	6.0	366	1	ML1A_SHEEP	P48040 ovis aries	1211	71.5	6.0	5303	2	Q9V628	Q9v628 drosophila
1139	71.5	6.0	369	2	Q70VF8	Q70vf8 sorex minut	1212	71	5.9	114	2	Q25269	Q25269 helicobacte
1140	71.5	6.0	369	2	CAD59501	Cad59501 sorex min	1213	71	5.9	150	2	Q82ZC0	Q82zco enterococcu
1141	71.5	6.0	375	2	Q6RKP7	Q6rkp7 human herpe	1214	71	5.9	150	2	Q8U3Q3	Q8u3q3 pyrococcus
1142	71.5	6.0	375	2	AAT01422	Aat01422 human her	1215	71	5.9	173	2	Q9WD21	Q9wd21 equine arte
1143	71.5	6.0	379	1	CYB_OCHCO	Q953j5 ochotona co	1216	71	5.9	188	1	5H2A_CANFA	Q46635 canis fami
1144	71.5	6.0	379	1	CYB_OCHFO	Q9gbv5 ochotona fo	1217	71	5.9	195	2	Q6MTK4	Q6mtk4 mycoplasma
1145	71.5	6.0	379	1	CYB_SORRA	Q79462 sorex radde	1218	71	5.9	195	2	CAE77032	Caet77032 mycoplas
1146	71.5	6.0	379	1	CYB_SPEPA	Q9tf55 spermophilu	1219	71	5.9	199	2	Q8THM3	Q8thm3 methanosaar
1147	71.5	6.0	379	2	Q48007	Q48007 perognathus	1220	71	5.9	199	2	Q8THM3	Q8thm3 methanosaar
1148	71.5	6.0	379	2	Q7IBW1	Q7ibw1 glaucomy s	1221	71	5.9	200	2	Q85JU8	Q85ju8 ceratobaeus
1149	71.5	6.0	379	2	Q34661	Q34661 glaucomy s	1222	71	5.9	200	2	Q9J7J9	Q9j7j9 porcine rep
1150	71.5	6.0	379	2	Q9TF66	Q9tf66 spermophilu	1223	71	5.9	219	2	Q93ID2	Q93id2 staphylococ
1151	71.5	6.0	379	2	Q952R3	Q952r3 glaucomy s	1224	71	5.9	223	2	Q91NK5	Q91nk5 avian infec
1152	71.5	6.0	379	2	Q8W8K3	Q8w8k3 thomomys ta	1225	71	5.9	223	2	Q91NK6	Q91nk6 avian infec
1153	71.5	6.0	381	2	Q8ZXPF	Q8zxp7 pyrobaculum	1226	71	5.9	223	2	Q91S96	Q91s96 avian infec
1154	71.5	6.0	381	2	Q79571	Q79571 mustelus ma	1227	71	5.9	223	2	Q91S96	Q91s96 avian infec
1155	71.5	6.0	381	2	Q6RKP4	Q6rkp4 human herpe	1228	71	5.9	225	1	VME1_IBVK	P12649 avian infec
1156	71.5	6.0	381	2	AAT01425	Aat01425 human her	1229	71	5.9	225	2	Q6R4P1	Q6r4p1 avian infec
1157	71.5	6.0	382	2	Q9NYN8	Q9ny8 homo sapien	1230	71	5.9	225	2	Q7T8G9	Q7tes9 avian infec
1158	71.5	6.0	383	1	YIY4_SCHPO	Q9uu18 schizosacch	1231	71	5.9	225	2	AAS00084	Aas00084 avian inf
1159	71.5	6.0	386	1	OXYR_PIG	P32306 sus scrofa	1232	71	5.9	226	2	Q7T405	Q7t405 avian infec
1160	71.5	6.0	386	2	Q8RB76	Q8rb76 thermoanaer	1233	71	5.9	234	2	Q9F6V0	Q9f6v0 bacteroides
1161	71.5	6.0	388	2	Q8S091	Q8sg91 nycteris th	1234	71	5.9	238	1	PYRF_BACAN	O81wf5 bacillus an
1162	71.5	6.0	388	2	Q8S093	Q8sg93 nycteris gr	1235	71	5.9	238	2	Q9T4G5	O9t4g5 phlebotomus
1163	71.5	6.0	390	1	ITR_CATCO	Q90334 catotomus	1236	71	5.9	238	2	Q9T8W9	Q9tes9 phlebotomus
1164	71.5	6.0	392	2	Q9AH88	Q9ah88 streptococc	1237	71	5.9	238	2	Q9XMR4	Q9xm4 phlebotomus
1165	71.5	6.0	407	2	Q6DGO1	Q6dgo1 brachydanio	1238	71	5.9	238	2	Q9XMR4	Q9xm4 phlebotomus
1166	71.5	6.0	410	2	Q82AH6	Q82ah6 streptomyc	1239	71	5.9	238	2	AAT33139	Aat33139 bacillus
1167	71.5	6.0	418	2	Q7NKE2	Q7nke2 gloeobacter	1240	71	5.9	243	2	Q34969	Q34969 myrmecia ba
1168	71.5	6.0	419	2	Q7VAC4	Q7vac4 prochloroco	1241	71	5.9	244	2	Q74HS0	Q74hs0 lactobacill
1169	71.5	6.0	435	2	Q891I7	Q89i17 bradyrhizob	1242	71	5.9	244	2	AAS09620	Aas09620 lactobaci
1170	71.5	6.0	435	2	Q929P5	Q929p5 listeria in	1243	71	5.9	250	2	Q9KVVQ3	Q9kvq3 vibrio chol
1171	71.5	6.0	435	2	Q8Y5E0	Q8y5e0 listeria mo	1244	71	5.9	255	2	Q66484	Q66484 equine arte
1172	71.5	6.0	435	2	Q71XN9	Q71xn9 listeria mo	1245	71	5.9	258	2	Q9PP98	Q9pp98 campylobact
1173	71.5	6.0	435	2	AAT04926	Aat04926 listeria	1246	71	5.9	266	2	Q6W249	Q6w249 rhizobium s
1174	71.5	6.0	466	2	Q89EQ8	Q89eq8 bradyrhizob	1247	71	5.9	266	2	AAQ87169	Aaq87169 rhizobium
1175	71.5	6.0	470	2	Q05351	Q05351 entamoeba h	1248	71	5.9	277	2	Q70NW1	Q70nw1 strongyloid
1176	71.5	6.0	501	2	Q9XH61	Q9xh61 matricaria	1249	71	5.9	277	2	CAD90566	Cad90566 strongylo
1177	71.5	6.0	501	2	Q6DB53	Q6db53 erwinia car	1250	71	5.9	279	2	Q7NEM0	Q7nbm0 mycoplasma
1178	71.5	6.0	510	1	HEX6_RICCO	Q07423 ricinus com	1251	71	5.9	281	2	Q8SK19	Q8sk19 necator ame
1179	71.5	6.0	518	2	Q880G3	Q880g3 pseudomonas	1252	71	5.9	289	2	Q8HZF2	Q8hzf2 macaca ap.
1180	71.5	6.0	521	2	Q6CVF0	Q6cvf0 kluyveromyc	1253	71	5.9	290	1	CB4A_ARATH	Q07473 arabidopsis
1181	71.5	6.0	524	2	Q80905	Q80905 arabidopsis	1254	71	5.9	295	2	Q8P0V2	Q8p0v2 streptococc
1182	71.5	6.0	524	2	Q6NHES5	Q6nhes5 corynebacte	1255	71	5.9	295	2	Q9ZG33	Q9z9g3 streptococc
1183	71.5	6.0	524	2	CAE49720	Caet49720 coryneb	1256	71	5.9	295	2	Q7CF29	Q7cf29 streptococc
1184	71.5	6.0	536	2	Q81F50	Q81f50 bacillus ce	1257	71	5.9	295	2	Q7CN71	Q7cn71 streptococc
1185	71.5	6.0	550	2	Q8VMK1	Q8vmk1 pseudomonas	1258	71	5.9	308	1	SG12_CAEEL	P46564 caenorhabdi
1186	71.5	6.0	550	2	Q881M5	Q88im5 pseudomonas	1259	71	5.9	310	1	Y160_BUCAP	Q8k9x4 buchnera ap
1187	71.5	6.0	603	2	Q6G6A7	Q6g6a7 staphylococ	1260	71	5.9	325	2	Q9NNR9	Q9nnr9 tamias stri
1188	71.5	6.0	603	2	Q6GDN2	Q6gdn2 staphylococ	1261	71	5.9	343	2	Q7YF04	Q7yfu4 myrmica kar
1189	71.5	6.0	603	2	Q99R71	Q99r71 staphylococ	1262	71	5.9	345	2	Q78911	Q78911 anolis occu
1190	71.5	6.0	603	2	Q792V2	Q792v2 staphylococ	1263	71	5.9	361	2	Q98PJ1	Q98pj1 mycoplasma
1191	71.5	6.0	603	2	Q7A3D6	Q7a3d6 staphylococ	1264	71	5.9	374	2	Q71EA5	Q71ea5 galerella s
1192	71.5	6.0	651	2	Q9M2X4	Q9m2x4 arabidopsis	1265	71	5.9	374	2	AAQ08835	Aaq08835 galerella
1193	71.5	6.0	669	1	YH06_HABIN	P45335 haemophilus	1266	71	5.9	379	1	CYB_CRATY	Q8wdul cratogeomys
1194	71.5	6.0	670	1	S1A2_RAT	P46720 rattus norv	1267	71	5.9	379	1	CYB_THOUM	Q47993 thomomys um
1195	71.5	6.0	725	1	Q7Z4M8	Q7z4m8 homo sapien	1268	71	5.9	379	2	O47979	O47979 thomomys bo
1196	71.5	6.0	725	1	MTRR_HUMAN	Q9ubk8 homo sapien	1269	71	5.9	379	2	O47981	O47981 thomomys bo
1197	71.5	6.0	743	2	Q8GT52	Q8gt52 hordeum vul	1270	71	5.9	379	2	Q6QX63	Q6qx63 urseus thibe
1198	71.5	6.0	814	2	Q23141	Q23141 caenorhabdi	1271	71	5.9	379	2	Q9TF00	Q9tf00 geomys bure
1199	71.5	6.0	838	2	Q8DG40	Q8dg40 vibrio vuln	1272	71	5.9	379	2	Q9TF03	Q9tf03 geomys bure

1273	71	5.9	379	2	Q8W7H1	Q8w7h1 thomomys ma	1346	71	5.9	2304	2	Q9BMQ4	Q9bmq4 blattella g
1274	71	5.9	379	2	AAT06913	Aat06913 ursus thi	1347	71	5.9	2423	2	Q77393	Q77393 plasmodium
1275	71	5.9	380	2	O03396	O03396 acomyx sp.	1348	71	5.9	2681	2	Q95V80	Q95v80 strongyloce
1276	71	5.9	380	2	O03397	O03397 acomyx sp.	1349	71	5.9	3010	2	Q68285	Q68285 hepatitis c
1277	71	5.9	380	2	Q9T502	Q9t502 geomys brev	1350	71	5.9	3010	2	Q81541	Q81541 hepatitis c
1278	71	5.9	380	2	Q9T576	Q9t576 acomyx sp.	1351	71	5.9	3010	2	Q81825	Q81825 hepatitis c
1279	71	5.9	380	2	Q9T577	Q9t577 thomomys bo	1352	71	5.9	3010	2	Q9DTE5	Q9dte5 hepatitis c
1280	71	5.9	380	2	Q6E3J7	Q6e3j7 thomomys bo	1353	70.5	5.9	203	1	BCRC_BACLI	P42334 bacillus li
1281	71	5.9	380	2	Q8EW1	Q8emj1 oceanobacil	1354	70.5	5.9	203	2	AAD21215	Aad21215 bacillus
1282	71	5.9	381	1	CYB_PHAEL	Q35409 phascogale	1355	70.5	5.9	206	2	Q72LX2	Q72lx2 leptospira
1283	71	5.9	391	2	Q8RLY8	Q8rly8 salmonella	1356	70.5	5.9	206	2	AAS71961	Aas71961 leptospir
1284	71	5.9	391	2	Q8RSF4	Q8rsf4 salmonella	1357	70.5	5.9	208	2	Q6BHB0	Q6bbh0 debaromyce
1285	71	5.9	391	2	Q9CGL8	Q9cgl8 lactococcus	1358	70.5	5.9	213	2	Q98E85	Q98e85 rhizobium l
1286	71	5.9	401	2	Q8S055	Q8s055 oryza sativ	1359	70.5	5.9	214	2	Q6GK20	Q6gk20 staphylococ
1287	71	5.9	403	2	Q8ZPR2	Q8zpr2 salmonella	1360	70.5	5.9	216	2	Q6VRP1	Q6vrp1 helicobacte
1288	71	5.9	403	2	Q9F2J6	Q9f2j6 streptomyce	1361	70.5	5.9	216	2	AAR03894	Aar03894 helicobac
1289	71	5.9	409	2	Q9ABC8	Q9abc8 caulobacter	1362	70.5	5.9	226	2	O03371	O03371 dipodomys o
1290	71	5.9	416	2	Q6QFBC	Q6qfbc legionella	1363	70.5	5.9	226	2	Q6DHQ1	Q6dhn1 brachydanio
1291	71	5.9	418	2	Q6QFBC	Q6qfbc legionella	1364	70.5	5.9	235	2	Q74888	Q74888 schizosacch
1292	71	5.9	418	2	Q6QFC1	Q6qfc1 legionella	1365	70.5	5.9	266	2	Q7CUF1	Q7cuf1 agrobacteri
1293	71	5.9	418	2	Q6QFC2	Q6qfc2 legionella	1366	70.5	5.9	266	2	Q8U854	Q8u854 agrobacteri
1294	71	5.9	418	2	Q6QFC4	Q6qfc4 legionella	1367	70.5	5.9	266	2	Q8U854	Q8u854 cooperia on
1295	71	5.9	418	2	Q6QFC6	Q6qfc6 legionella	1368	70.5	5.9	278	2	Q8YMW2	Q8ymw2 anabaena sp
1296	71	5.9	418	2	AAS92180	Aas92180 legionell	1369	70.5	5.9	283	2	Q9A290	Q9a290 lactobacill
1297	71	5.9	418	2	AAS92182	Aas92182 legionell	1370	70.5	5.9	285	2	Q7S2B8	Q7s2b8 neurospora
1298	71	5.9	418	2	AAS92184	Aas92184 legionell	1371	70.5	5.9	285	2	CAE76167	Caef76167 neurospor
1299	71	5.9	418	2	AAS92185	Aas92185 legionell	1372	70.5	5.9	290	2	Q6SGH2	Q6sgh2 uncultured
1300	71	5.9	418	2	AAS92186	Aas92186 legionell	1373	70.5	5.9	290	2	AAR37890	Aar37890 unculture
1301	71	5.9	418	2	AAS92190	Aas92190 legionell	1374	70.5	5.9	291	2	Q37789	Q37789 helianthus
1302	71	5.9	419	2	Q95Q81	Q95q81 caenorhabdi	1375	70.5	5.9	292	2	Q746W1	Q746w1 geobacter s
1303	71	5.9	423	2	Q8Y5H6	Q8y5h6 listeria mo	1376	70.5	5.9	292	2	Q746W1	Q746w1 geobacter s
1304	71	5.9	438	2	Q6I5Y4	Q6i5y4 oryza sativ	1377	70.5	5.9	292	2	Q746W1	Q746w1 geobacter s
1305	71	5.9	442	2	Q96ZK3	Q96zk3 sulfolobus	1378	70.5	5.9	312	2	Q6CEC0	Q6cec0 yarrowia li
1306	71	5.9	448	2	P91683	P91683 drosophila	1379	70.5	5.9	312	2	Q6CEC0	Q6cec0 yarrowia li
1307	71	5.9	451	2	Q9SNW3	Q9snw3 vernicia fo	1380	70.5	5.9	315	2	Q9JK65	Q9jk65 rattus norv
1308	71	5.9	451	2	Q9F992	Q9f992 buchnera ap	1381	70.5	5.9	315	2	Q9JK65	Q9jk65 rattus norv
1309	71	5.9	470	1	SH2A_PIG	P50129 sus scrofa	1382	70.5	5.9	320	2	Q7N0S0	Q7n0s0 photorhabdu
1310	71	5.9	471	1	SH2A_HUMAN	P28223 homo sapien	1383	70.5	5.9	326	2	Q9BF39	Q9bf39 manis penta
1311	71	5.9	471	2	AAH65356	Aah65356 homo sapi	1384	70.5	5.9	326	2	Q9BF39	Q9bf39 manis penta
1312	71	5.9	471	2	AAH69576	Aah69576 homo sapi	1385	70.5	5.9	335	2	Q9Z131	Q9z131 elephanthulu
1313	71	5.9	472	2	Q6KI36	Q6ki36 mycoplasma	1386	70.5	5.9	335	2	Q9Z131	Q9z131 elephanthulu
1314	71	5.9	472	2	AAT27740	Aat27740 mycoplasma	1387	70.5	5.9	336	2	Q9THE3	Q9the3 sorx pacif
1315	71	5.9	480	2	Q73CA7	Q73ca7 bacillus ce	1388	70.5	5.9	336	2	Q9THE3	Q9the3 sorx pacif
1316	71	5.9	480	2	RAA540089	Aas40089 bacillus	1389	70.5	5.9	336	2	Q9THE3	Q9the3 sorx pacif
1317	71	5.9	485	2	Q9CL47	Q9cl47 pasteurella	1390	70.5	5.9	336	2	Q9THE3	Q9the3 sorx pacif
1318	71	5.9	485	2	Q8SHR0	Q8shr0 trichoderma	1391	70.5	5.9	340	2	Q55632	Q55632 synchocyst
1319	71	5.9	489	2	Q8SHR0	Q8shr0 trichoderma	1392	70.5	5.9	340	2	Q55632	Q55632 synchocyst
1320	71	5.9	545	1	SOAL_RAT	Q7n9d9 photorhabdu	1393	70.5	5.9	343	2	Q7Y7B1	Q7y7b1 myrmica hir
1321	71	5.9	545	1	MUP3_YEAST	Q7o536 rattus norv	1394	70.5	5.9	343	2	Q7Y7B1	Q7y7b1 myrmica hir
1322	71	5.9	546	1	Q8I3H5	P38734 saccharomyc	1395	70.5	5.9	343	2	Q7Y7B1	Q7y7b1 myrmica hir
1323	71	5.9	548	2	Q8AUN9	Q8aun9 fugu rubrip	1396	70.5	5.9	350	2	Q9X370	Q9x370 homo sapien
1324	71	5.9	554	2	Q8AUN9	Q8aun9 fugu rubrip	1397	70.5	5.9	351	2	Q9X370	Q9x370 homo sapien
1325	71	5.9	563	1	YAS8_SCHPO	Q10144 schizosacch	1398	70.5	5.9	352	2	Q9R808	Q9r808 mycoplasma
1326	71	5.9	564	1	S229_MOUSE	Q9wtm6 mus musculu	1399	70.5	5.9	352	2	Q9R808	Q9r808 mycoplasma
1327	71	5.9	564	2	Q6F1V1	Q6flv1 mesoplasma	1400	70.5	5.9	353	2	Q9GCR9	Q9gcr9 glaucumys v
1328	71	5.9	576	1	OCT1_CABEL	Q9u539 caenorhabdi	1401	70.5	5.9	353	2	Q9GCR9	Q9gcr9 glaucumys v
1329	71	5.9	584	1	LYTS_STAAU	Q53705 staphylococ	1402	70.5	5.9	353	2	Q7TN44	Q7tn44 rattus norv
1330	71	5.9	615	2	Q7R950	Q7r950 plasmodium	1403	70.5	5.9	356	2	Q9GCR9	Q9gcr9 glaucumys v
1331	71	5.9	620	2	Q8Z2J7	Q8z2j7 cyanidiosch	1404	70.5	5.9	360	2	Q8H1B8	Q8hib8 callosciuru
1332	71	5.9	631	2	Q8I2W0	Q8i2w0 homo sapien	1405	70.5	5.9	360	2	Q8H1B8	Q8hib8 callosciuru
1333	71	5.9	676	2	O04521	Q04521 arabidopsis	1406	70.5	5.9	361	2	Q8H1C3	Q8hic3 callosciuru
1334	71	5.9	701	2	Q8EWL9	Q8ewl9 mycoplasma	1407	70.5	5.9	361	2	Q8H1C3	Q8hic3 callosciuru
1335	71	5.9	762	2	Q8ML23	Q8ml23 drosophila	1408	70.5	5.9	361	2	Q8H1C3	Q8hic3 callosciuru
1336	71	5.9	788	2	Q8ZJB7	Q8zjb7 helicobacte	1409	70.5	5.9	363	2	Q7BYC0	Q7byc0 bacillus ce
1337	71	5.9	826	2	Q8TQ61	Q8tqx6 methanosarc	1410	70.5	5.9	363	2	Q7BYC0	Q7byc0 bacillus ce
1338	71	5.9	885	2	Q75BGL	Q75bgl ashbya goss	1411	70.5	5.9	366	2	Q9K337	Q9k337 bacillus ce
1339	71	5.9	885	2	AAS1521	Aas1521 ashbya go	1412	70.5	5.9	366	2	Q6TTN3	Q6ttn3 homo sapien
1340	71	5.9	913	2	O13099	O13099 xenopus lae	1413	70.5	5.9	366	2	Q6TTN3	Q6ttn3 homo sapien
1341	71	5.9	932	2	Q84Z07	Q84zg7 oryza sativ	1414	70.5	5.9	369	2	Q70VB2	Q70vb2 sorx volnu
1342	71	5.9	964	2	Q84Z07	Q84zg7 oryza sativ	1415	70.5	5.9	369	2	CAD59544	Cad59544 sorx volnu
1343	71	5.9	1239	2	Q8SC10	Q8scl0 neurospora	1416	70.5	5.9	369	2	Q6VPS4	Q6vps4 canis fami
1344	71	5.9	1242	2	Q8CBAL	Q8cbal yarrowia li	1417	70.5	5.9	370	2	Q6VPS4	Q6vps4 canis fami
1345	71	5.9	1409	2	Q7T9B1	Q7t9b1 human cytom	1418	70.5	5.9	370	2	AAR03486	Aar03486 canis fam
					Q7xw92 oryza sativ								

1419	70.5	5.9	379	2	Q9GAW5	Q9gaw5 dipodomys e
1420	70.5	5.9	379	2	Q9GBY3	Q9gby3 ochotona da
1421	70.5	5.9	379	2	Q8W9L6	Q8w9l6 glaucomyx v
1422	70.5	5.9	382	2	Q9HIJ9	Q9hi j9 thermoplasm
1423	70.5	5.9	386	2	Q6RKP3	Q6rkp3 human herpe
1424	70.5	5.9	386	2	AAT01426	Aat01426 human her
1425	70.5	5.9	387	1	T2C_PARTE	Q27181 paramacium
1426	70.5	5.9	389	1	MTR_BUFMA	Q90252 bufo marinu
1427	70.5	5.9	390	1	PE23_HUMAN	P43115 homo sapien
1428	70.5	5.9	393	2	O00326	O00326 homo sapien
1429	70.5	5.9	393	2	AAR07903	Aar07903 homo sapi
1430	70.5	5.9	394	2	O8X1V7	O8x1v7 coriolus ve
1431	70.5	5.9	402	2	O00325	O00325 homo sapien
1432	70.5	5.9	403	2	Q9KGI1	Q9kgi1 mycoplasma
1433	70.5	5.9	414	2	Q6Z9G4	Q6z9g4 oryza sativ
1434	70.5	5.9	414	2	BAD09897	Bad09897 oryza sat
1435	70.5	5.9	414	2	BAD09911	Bad09911 oryza sat
1436	70.5	5.9	416	2	O6VPS5	O6vps5 canis famil
1437	70.5	5.9	416	2	AAR03485	Aar03485 canis fam
1438	70.5	5.9	420	2	Q7BR79	Q7br79 aeromonas p
1439	70.5	5.9	420	2	AAS66623	Aas66623 aeromonas
1440	70.5	5.9	423	2	O58964	O58964 pyrococcus
1441	70.5	5.9	424	2	Q7VF09	Q7vf09 helicobacte
1442	70.5	5.9	436	2	O6BUT5	O6but5 debaryomyce
1443	70.5	5.9	440	1	CAPE_STAUA	P39854 staphylococ
1444	70.5	5.9	452	2	Q83C47	Q83c47 coxiella bu
1445	70.5	5.9	460	2	Q7VIT8	Q7vit8 helicobacte
1446	70.5	5.9	470	2	Q6SED7	Q6sed7 lactobacill
1447	70.5	5.9	470	2	AAR27374	Aar27374 lactobaci
1448	70.5	5.9	470	2	AAS09206	Aas09206 lactobaci
1449	70.5	5.9	472	2	Q9LCN5	Q9lcn5 micromonosp
1450	70.5	5.9	472	2	O8YCN7	O8ycn7 bruceella me
1451	70.5	5.9	496	2	O25600	O25600 helicobacte
1452	70.5	5.9	496	2	O8CQ64	O8cq64 staphylococ
1453	70.5	5.9	500	2	O8EQ01	O8eq01 oceanobacil
1454	70.5	5.9	508	2	Q7RQV6	Q7rqv6 plasmodium
1455	70.5	5.9	521	1	CYOA_HAEIN	P45021 haemophilus
1456	70.5	5.9	536	1	WVIN_CHLMU	Q9pjb9 chlamydia m
1457	70.5	5.9	556	2	Q22109	Q22109 caenorhabdi
1458	70.5	5.9	556	2	Q7VH12	Q7vh12 helicobacte
1459	70.5	5.9	558	2	O6E1C5	O6eic5 perkinsus m
1460	70.5	5.9	574	1	RFT1_YEAST	P38206 saccharomyc
1461	70.5	5.9	585	2	Q7R1V4	Q7r1v4 giardia lam
1462	70.5	5.9	598	1	S6A1_MUSCO	P48057 mus cookii
1463	70.5	5.9	599	1	S6A1_MOUSE	P31648 mus musculu
1464	70.5	5.9	599	1	S6A1_RAT	P23978 rattus norv
1465	70.5	5.9	599	2	O8N4K8	O8n4k8 homo sapien
1466	70.5	5.9	633	2	Q7QS02	Q7qs02 giardia lam
1467	70.5	5.9	641	2	Q7PMH7	Q7pmh7 anopheles g
1468	70.5	5.9	658	2	Q7ZUF5	Q7zuf5 brachydanio
1469	70.5	5.9	662	1	T9S2_MOUSE	P58021 mus musculu
1470	70.5	5.9	662	2	O8C6H4	O8c6h4 mus musculu
1471	70.5	5.9	662	2	O8C7F9	O8c7f9 mus musculu
1472	70.5	5.9	662	2	BAC33215	Bac33215 mus muscu
1473	70.5	5.9	662	2	BAC40645	Bac40645 mus muscu
1474	70.5	5.9	667	2	Q9G864	Q9g864 malawimonas
1475	70.5	5.9	676	2	Q7Q1I4	Q7ql14 anopheles g
1476	70.5	5.9	676	2	Q7RNV6	Q7rnv6 plasmodium
1477	70.5	5.9	679	2	Q7Q645	Q7q645 anopheles g
1478	70.5	5.9	683	2	Q972H7	Q972h7 sulfolobus
1479	70.5	5.9	689	2	Q72YU0	Q72yu0 bacillus ce
1480	70.5	5.9	689	2	AAS43831	Aas43831 bacillus
1481	70.5	5.9	700	2	Q9LDT0	Q9ldt0 arabidopsis
1482	70.5	5.9	717	2	O6NHL8	O6nhl8 corynebacte
1483	70.5	5.9	717	2	CAE49638	Caе49638 corynebac
1484	70.5	5.9	729	2	Q8ESC5	Q8esc5 oceanobacil
1485	70.5	5.9	740	2	Q7XCM9	Q7xcm9 oryza sativ
1486	70.5	5.9	740	2	Q9FRK0	Q9frk0 oryza sativ
1487	70.5	5.9	766	2	Q9L230	Q9l230 arabidopsis
1488	70.5	5.9	769	2	O7MLT5	O7mlt5 bordetella
1489	70.5	5.9	776	1	CHS1_CANAL	P23316 candida alb
1490	70.5	5.9	856	2	Q9FHV2	Q9fhv2 arabidopsis
1491	70.5	5.9	899	2	Q9FFI4	Q9ffi4 arabidopsis
1492	70.5	5.9	951	2	Q6PK21	Q6fk21 candida gla
1493	70.5	5.9	980	2	Q8A3J1	Q8a3j1 bacteroides
1494	70.5	5.9	1026	2	Q9URM1	Q9urm1 candida alb
1495	70.5	5.9	1199	2	Q9Y4J9	Q9y4j9 homo sapien
1496	70.5	5.9	1234	2	Q8VD34	Q8vd34 mus musculu
1497	70.5	5.9	1491	2	O7S5P1	O7s5p1 neurospora
1498	70.5	5.9	1583	2	Q92GE9	Q92ge9 rickettsia
1499	70.5	5.9	1764	2	Q8MUA3	Q8mua3 strongyloce
1500	70.5	5.9	1781	1	AK12_HUMAN	Q02952 homo sapien

ALIGNMENTS

RESULT 1

MENT_HUMAN

ID_MENT_HUMAN

STANDARD;

PRT;

234

AA.

AC

O95772;

DT

28-FEB-2003 (Rel. 41, Created)

DT

28-FEB-2003 (Rel. 41, Last sequence update)

DT

05-JUL-2004 (Rel. 44, Last annotation update)

DE

MLN64 N-terminal domain homolog (STARD3 N-terminal like protein)

DE

(UNQ855/PRO1864).

GN

Name=STARD3NL; Synonyms=MENTHO;

OS

Homo sapiens (Human).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBI_TaxID=9606;

RN

[1]

RP

SEQUENCE FROM N.A. CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND

RP

ALTERNATIVE INITIATION.

RC

TISSUE=Fetal brain;

RX

MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;

RA

Alpy F., Wendling C., Rio M.-C., Tomasetto C.;

RT

"MENTHO, a MLN64 homologue devoid of the START domain.";

RL

J. Biol. Chem. 277:50780-50787(2002).

RN

[2]

RP

SEQUENCE FROM N.A.

RP

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

RA

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA

Godowski P., Gray A.;

RT

"The secreted protein discovery initiative (SPDI), a large-scale

RT

effort to identify novel human secreted and transmembrane proteins: a

RT

bioinformatics assessment.";

RL

Genome Res. 13:2265-2270(2003).

RN

[3]

RP

SEQUENCE FROM N.A.

RP

Arnett C., Wohldmann P., Le T.;

RL

Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.

RN

[4]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Brain, and Kidney;

RX

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA

Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA

Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA

Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC alternative initiation;
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: Contains 1 MENTAL domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ492267; CAD37353.1; -
CC EMBL; AY358645; AAQ89008.1; -
CC EMBL; AC006033; AAQ07552.1; -
CC EMBL; BC003074; AAHQ3074.1; -
CC EMBL; BC005959; AAHQ5959.1; -
CC Genbank; HGNC:19169; STARD3NL.
CC
CC Alternative initiation; Phosphorylation; Transmembrane.
CC
CC MLN64 N-terminal domain homolog, isoform
CC CHAIN 1 234
CC
CC CHAIN 8 234
CC
CC INIT MET 8
CC DOMAIN 48
CC TRANS 1 53
CC TRANS 54 74
CC TRANS 75 97
CC TRANS 98 118
CC TRANS 119 122
CC TRANS 123 143
CC TRANS 144 150
CC TRANS 151 171
CC TRANS 172 234
CC SEQUENCE 234 AA; 26654 MW; AFE7DAE381983FB0 CRC64;
CC
CC Query Match 100.0%; Score 1195; DB 1; Length 234;
CC Best Local Similarity 100.0%; Pred. No. 3e-100;
CC Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 MNHLPEDMENALTSQSSHASLRNTHSNPTQLMARIESYGRKKGISDVRRTFCFLVPT 60
CC Db 1 MNHLPEDMENALTSQSSHASLRNTHSNPTQLMARIESYGRKKGISDVRRTFCFLVPT 60
CC QY 61 FDLLEVTLLWIELNVNGGIENTLEKEVMQYDIYSSYDFIPELLAVFRPKVILAYAVCRL 120
CC Db 61 FDLLEVTLLWIELNVNGGIENTLEKEVMQYDIYSSYDFIPELLAVFRPKVILAYAVCRL 120
CC QY 121 RHWMAIALTAVTSALAKVILSKLFSQAGFYVLPILSIILAWIETWFLDFKVLPOEA 180
CC Db 121 RHWMAIALTAVTSALAKVILSKLFSQAGFYVLPILSIILAWIETWFLDFKVLPOEA 180
CC QY 181 EENRLLIVQDASERAAALIPGLSDGQFYSPSEAGSEAEKQDSKPLLEL 234
CC Db 181 EENRLLIVQDASERAAALIPGLSDGQFYSPSEAGSEAEKQDSKPLLEL 234
CC
CC RESULT 2
CC MENT_MOUSE
CC ID MENT_MOUSE STANDARD; PRT; 235 AA.
CC AC Q9DCI3; Q99J63; Q9D356;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE MLN64 N-terminal domain homolog (STARD3 N-terminal like protein).
GN Name=Stard3n1; Synonyms=Menthos;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9DCI3-1; Sequence=Displayed;
CC Name=2;


```

CC      IsoId=O9DCI3-2; Sequence=VSP 003909;
CC      Note=No experimental confirmation available;
CC      -!- SIMILARITY: Contains 1 MENTAL domain.
CC      -!- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
CC      a frameshift in position 31.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      modified and this statement is not removed. Usage by and for commercial
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AK002760; BAB22337.1; -.
DR      EMBL; AK018331; BAB31166.1; ALT_FRAME.
DR      EMBL; BC003334; AAH03334.1; -.
DR      MGD; MGI:1923455; Stard3n1.
KW      Alternative splicing; Transmembrane.
FT      DOMAIN 48 218
FT      DOMAIN 1 53
FT      TRANSMEM 54 74
FT      DOMAIN 75 97
FT      TRANSMEM 98 118
FT      DOMAIN 119 122
FT      TRANSMEM 123 143
FT      DOMAIN 144 150
FT      TRANSMEM 151 171
FT      DOMAIN 172 235
FT      VARSPLIC 218 235
FT      FTId=VSP 003909.
FT      QI -> HS (in Ref. 1; BAB22337).
FT      R -> G (in Ref. 2).
FT      SEQUENCE 235 AA; 26811 MW; P251725390CB1503 CRC64;
Query Match 94.9%; Score 1134.5; DB 1; Length 235;
Best Local Similarity 94.9%; Pred. No. 9.5e-95;
Matches 223; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 1 MNHLPEDMENALTGSSQSSHASLRNIHSINPTQMARIYESGEGREKKGISDVRRFTCLFVFT 60
DB 1 MNHLPEDMENALTGSSQSSHASLRDIHSINPAQLMARIYESGEGREKKGISDVRRFTCLFVFT 60
QY 61 FDLFLVTLMIELNVNGGIENTLEKEVMQYDYSSYDFIPLAVFRFKVLIILAYAVCRL 120
DB 61 FDLFLVTLMIELNVNGGIENTLEKEVHYDYSSYDFIPLAVFRFKVLIILGYAVCRL 120
QY 121 RHWMAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPILISFILAWIETWFLDFKVLPOEA 180
DB 121 RHWMAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPILISFILAWIETWFLDFKVLPOEA 180
QY 181 EENRLLIVQDASRAALI-PGGLSDGQFYSPPESEAGS-BEAEKQDSEKPLLEL 234
DB 181 EENRLLIVQDASRAALI-PGGLSDGQFYSPPESEAGS-BEAEKQDSEKPLLEL 235
RESULT 3
Q6DI38 PRELIMINARY; PRT; 227 AA.
AC Q6DI38;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC      TISSUE=Embryo;
RC      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Vallalal D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;
Query Match 66.6%; Score 796; DB 2; Length 227;
Best Local Similarity 68.3%; Pred. No. 5e-64;
Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;
QY 8 MENALTGSSQSSHASLRNIHSINPTQMARIYESGEGREKKGISDVRRFTCLFVFT 67
DB 1 MDSQCSSSVGSRRANLGGINSTPI SARVESAGEKKGISDVRRFTCLFVFT 60
QY 68 LLMIELNVNGGIENTLEKEVMQYDYSSYDFIPLAVFRFKVLIILAYAVCRLRHWMAIA 127
DB 61 LLMIELNVNGGIIQQOLEQVLYDKHSFDFIPLAVFRFAALILAYAVCRLRHWMAIA 120
QY 128 LTTAVTSFAFLAKVILSKLFSQAGFYVLPILISFILAWIETWFLDFKVLPOEAEEENRLL 187
DB 121 ITTAVTTGLIVKVVVSKLSQAGFYVLPILISFILAWIETWFLDFKVLPOEADEIRYL 180
QY 188 IVQDASRAALI-PGGLSDGQFYSPPESEAGS-BEAEKQDSEKPLL 232
DB 181 SVQNRLEHEPLPPGLSEGLFYSPPESEAGS-BEAEKQDSEKPLV 227
RESULT 4
Q6DFR7 PRELIMINARY; PRT; 448 AA.
AC Q6DFR7;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076666; AAH76666.1; -.
KW Hypothetical protein.
SQ SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;
Query Match 58.6%; Score 700.5; DB 2; Length 448;
Best Local Similarity 61.1%; Pred. No. 5.3e-55;
Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;
QY 1 MNHLP-----EDMENALTGSSSHASLRNIHSINPTQMARISEYEGREKKGISDVRRTFC 56
DB 1 MTKLPGDFQPDRLERSLPAIASINSSQNVFSPHSLLP-----EQRRAISDVRRTFC 54
QY 57 LFTVFDLLFTLLWIIELNVNGGIENTLEKVMQDYVSYDFIFLLAVFRFKVLIILAYA 116
DB 55 LFTVFDLLFTLLWIIELNVNDGIEKLEELHYDFKNSFFDIFLLAVFRFSVLIILAYA 114
QY 117 VCLRLHWWAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPISFILAWIETWFLDPKVL 176
DB 115 IVRLHWWAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPISFVLAWLETWFLDPKVL 174
QY 177 PORAEEENRLLIVQDASERAALI-PCGLSDGQFVSPPESEAGEEAEKQDSEK 229
DB 175 TQEAEEERWYNVAQAGSHPPLLYNGALSDGQFYSPPESPAGSD--NEFDDEE 226
RESULT 5
Q6PF40 ID Q6PF40 PRELIMINARY; PRT; 444 AA.
AC Q6PF40;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68989 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057738; AAH57738.1; -.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; STAR.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057738; AAH57738.1; -.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; STAR.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;
Query Match 58.5%; Score 698.5; DB 2; Length 444;
Best Local Similarity 60.9%; Pred. No. 7.9e-55;
Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;
QY 1 MNHLPDMENALTGSSSHASLRNIHSINPTQMARISEYEGREKKGISDVRRTFC 60
DB 1 MTKIPGDFQPDRLERSLPAIASMSQSHVSPHSLLP-----EQRRAISDVRRTFC 54
QY 61 FDLFTVLLWIIELNVNGGIENTLEKVMQDYVSYDFIFLLAVFRFKVLIILAYAVCLR 120
DB 55 FDLFTVLLWIIELNVNGGIENTLEKVMQDYVSYDFIFLLAVFRFSVLIILAYAVCLR 114
QY 121 RHWMAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPISFILAWIETWFLDPKVL 180
DB 115 RHWMAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPISFVLAWLETWFLDPKVL 174
QY 181 EENRLLIVQDASERAALI-PCGLSDGQFVSPPESEAGEEAEKQDSEK 229
DB 175 EERWYIAQAATHPSLLYNGALSDGQFYSPPESPAGSD--NEFDDEE 222
RESULT 6
AAH57738 ID AAH57738 PRELIMINARY; PRT; 444 AA.
AC AAH57738;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68989 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;

DE domain-containing protein 3) (CAB1 protein).
GS Name-STAR3; Synonyms=MLN64, CAB1;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast Carcinoma;
RX MEDLINE=96039245; PubMed=7490069;
RA Tomasetto C., Regnier C., Moog-Lutz C., Mattei M.-G., Chenard M.-P.,
RA Lidereau R., Baeset P., Rio M.-C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17";
RL Genomics 28:367-376(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oesophageal carcinoma;
RX MEDLINE=97413641; PubMed=9270027;
RA Akiyama N., Sasaki H., Ishizuka T., Terada M.;
RA Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT method";
RL Cancer Res. 57:3548-3553(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, Skin, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Basak S.A., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RX MEDLINE=20264523; PubMed=10802740;
RA Teujishita Y., Hurley J.H.;
RT "Structure and lipid transport mechanism of a STAR-related domain.";
RL Nat. Struct. Biol. 7:408-414(2000).
RN [5]
RP TOPOLOGY
RX MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;
RA Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA Chénard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT "The steroidogenic acute regulatory protein homolog MLN64, a late
RT endosomal cholesterol-binding protein.";
RL J. Biol. Chem. 276:4261-4269(2001).
CC -1- FUNCTION: Binds and transports cholesterol. Promotes
CC -1- steroidogenesis in placenta and brain.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein.
CC -1- SIMILARITY: Contains 1 MENTAL domain.
CC -1- SIMILARITY: Contains 1 STAR domain.
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/MLN64ID202.html".

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CC or send an email to license@isb-sib.ch).

CC EMBL; X80198; CAA56489.1; -;
DR EMBL; D38255; BAA22525.1; -;
DR EMBL; BC008356; AAH08356.1; -;
DR EMBL; BC008747; AAH08747.1; -;
DR EMBL; BC025679; AAH25679.1; -;
DR PIR; I38027; I38027.
DR PDB; 1EM2; X-ray; A=216-444.
DR Genew; HGNC:17579; STARD3.
DR MIM; 607048; -;
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0008203; P:cholesterol metabolism; TAS.
DR GO; GO:0008339; P:mitochondrial transport; TAS.
DR GO; GO:0008202; P:steroid metabolism; TAS.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; STAR.
DR Pfam; PF01852; STAR; 1
DR PRINTS; PRO0978; STARPROTEIN.
DR SMART; SM00234; STAR; 1.
DR PROSITE; PS00848; STAR; 1.
DR 3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
KW Transmembrane; Transport.
FT DOMAIN 1 51 Cytoplasmic (Potential).
FT TRANSMEM 52 72 Potential.
FT DOMAIN 73 94 Extracellular (Potential).
FT TRANSMEM 95 115 Potential.
FT DOMAIN 116 120 Cytoplasmic (Potential).
FT TRANSMEM 121 141 Potential.
FT DOMAIN 142 148 Extracellular (Potential).
FT TRANSMEM 149 169 Potential.
FT DOMAIN 170 445 Cytoplasmic (Potential).
FT DOMAIN 46 217 MENTAL.
FT DOMAIN 230 443 START.
FT CONFLICT 117 117 Q -> R (in Ref. 3; AAH08356/AAH25679).
FT CONFLICT 216 216 G -> A (in Ref. 3; AAH25679).
FT HELIX 233 253
FT TURN 254 255
FT HELIX 256 258
FT STRAND 260 264
FT TURN 266 267
FT STRAND 270 276
FT TURN 277 279
FT STRAND 280 289
FT HELIX 293 299
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FT TURN 397 398
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FT STRAND 408 409
FT HELIX 416 440
FT TURN 441 442

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SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DDEF CRC64;
Query Match 55.6%; Score 664; DB 1; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.1e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

Qy 1 MNHLP-----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
Db 1 MSKLPRLTRDLERSLPAVASLSGSLSHSLPPPE-----KRAISDV 49

Qy 52 RRTFCFLVTDLLFVTLIIELNVNGGIENLEKEVMQDYDYSSYPDIFLLAVFRPKVL 111
Db 50 RRTFCFLVTDLLFISLLWIELNTGIRKMLEQEIQYNFKTSFPDIFVLAFFRPSGL 109

Qy 112 ILAYAVCRRLHWAIAUATVTSFAFLAKVILSKLFSQAGFYVLPILSIILAWIETWFL 171
Db 110 LLGAVVLQLRHWWVIAVTTLVSSAFLIVKVLSELLSKGAFGYLLPTVSPVLALETWFL 169

Qy 172 DFKVLPQEAEEENRLLIVQDASERAALI-PGILSDGQFYSPPESEAGSE-EAEKQDSEK 229
Db 170 DFKVLPQEAEEERYWYLAQAVARGPLFLFGALSEGQFYSPPESEAGSDNESDEEVAGKK 229

RESULT 9
AAP35610 PRELIMINARY; PRT; 445 AA.
AC AAP35610;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE START domain containing 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT06964; AAP35610.1;
SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DDEF CRC64;

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.1e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

Qy 1 MNHLP-----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
Db 1 MSKLPRLTRDLERSLPAVASLSGSLSHSLPPPE-----KRAISDV 49

Qy 52 RRTFCFLVTDLLFVTLIIELNVNGGIENLEKEVMQDYDYSSYPDIFLLAVFRPKVL 111
Db 50 RRTFCFLVTDLLFISLLWIELNTGIRKMLEQEIQYNFKTSFPDIFVLAFFRPSGL 109

Qy 112 ILAYAVCRRLHWAIAUATVTSFAFLAKVILSKLFSQAGFYVLPILSIILAWIETWFL 171
Db 110 LLGAVVLQLRHWWVIAVTTLVSSAFLIVKVLSELLSKGAFGYLLPTVSPVLALETWFL 169

Qy 172 DFKVLPQEAEEENRLLIVQDASERAALI-PGILSDGQFYSPPESEAGSE-EAEKQDSEK 229
Db 170 DFKVLPQEAEEERYWYLAQAVARGPLFLFGALSEGQFYSPPESEAGSDNESDEEVAGKK 229

RESULT 10
ML64 MOUSE
ID ML64_MOUSE STANDARD; PRT; 446 AA.
AC Q61542;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE MLN 64 protein (STAR-related lipid transfer protein 3) (STARD3) (START
DE domain-containing protein 3) (ES 64 protein).
GN Name:Stard3; Synonyms:Mln64, ES64;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96039245; PubMed=7490069;
RA Tomasetto C., Regnier C.H., Moog-Lutz C., Mattei M.-G., Chenard M.-P.,
RA Lidereau R., Basset P., Rio M.-C.;
RT Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17."
RL Genomics 28:367-376(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Binds and transports cholesterol. Promotes
CC steroidogenesis in placenta and brain (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein (By similarity).
CC -I- SIMILARITY: Contains 1 MENTAL domain.
CC -I- SIMILARITY: Contains 1 START domain.
CC -----
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CC or send an email to license@ebi.ac.uk).
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RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK030365; BAC26922.1;
 SQ SEQUENCE 107 AA; 12417 MW; 1B30DA6C81469089 CRC64;
 Query Match 41.2%; Score 492; DB 2; Length 107;
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 DB 1 MNHLPEDMENALTGSSQSHASLRNHSINPTQLMARIESYEGREKKGISDVRRTFCIFVT 60
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 DB 61 FDLFLVTLMIELNVNGGIENTLEKEVMQDYSSYFDIFL 102
 RESULT 15
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 ID Q7QIT3
 AC Q7QIT3
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AGCP3158 (Fragment).
 GN Name=agCGS2468; ORFNames=ENSANGG00000018959;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB0100807; EAA03945.1;
 DR GO; GO:0015485; F:cholesterol binding; IEA.
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro; IPR000799; START.
 DR InterPro; IPR002913; START.
 DR Pfam; PF01852; START; 2.
 DR PRINTS; PR00978; STARPROTEIN.
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 SQ SEQUENCE 568 AA; 62932 MW; ECBE3D361A05DF15 CRC64;
 Query Match 29.1%; Score 348; DB 2; Length 568;
 Best Local Similarity 36.6%; Pred. No. 7.2e-23;
 Matches 86; Conservative 45; Mismatches 72; Indels 32; Gaps 9;
 QY 13 TGSQSHASLRNHSINPTQLMAR--IESYEGREKKGISDVRRTFCIFVTFDLLFVTLW 70
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 QY 71 IIELNVNG-GIENTLEKEVMQDYSSYFDIFLAVFRFKVLILAYAVCHLHWAIALT 129
 DB 48 IICVITGDNVHIALQTVLHYTVYTSLFDVVTAALIRFLFLFYGLLSISHLVLALS 107
 QY 130 TAVTSAPLLAKVLISKLFS--QGAFGYVLPPIISFILAWIETWFLDFKVLPOEAEENRL 187
 DB 108 TTSSCAFLISKVFLYDWTATPQPVFVLLIVGSFVLANGEAWFLDCRVIPQERYARV 167
 QY 188 IVODASERAAIP-----GGLSD--GQYSPSPES--EAGSEAEKQDSE 228
 DB 168 AITNPGSMDARTPLLPFLSAMQGRTESTIGNFYSPFDSIHNSDDDDDEQDDE 222
 Search completed: January 24, 2005, 16:18:38
 Job time : 253 secs

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933	71.5	6.0	394	14	US-10-394-136-51	Sequence 51, Appl	1006	70.5	5.9	363	16	US-10-768-878-9	Sequence 9, Appl
934	71.5	6.0	405	15	US-10-424-599-149141	Sequence 149141,	1007	70.5	5.9	365	14	US-10-060-902-32	Sequence 32, Appl
935	71.5	6.0	410	14	US-10-156-761-13608	Sequence 13608, A	1008	70.5	5.9	365	14	US-10-354-247-32	Sequence 32, Appl
936	71.5	6.0	433	16	US-10-437-963-158065	Sequence 158065,	1009	70.5	5.9	366	10	US-09-992-331-9	Sequence 9, Appl
937	71.5	6.0	448	15	US-10-425-114-55760	Sequence 55760, A	1010	70.5	5.9	366	14	US-10-369-493-10462	Sequence 30, Appl
938	71.5	6.0	524	15	US-10-282-122A-53957	Sequence 53957, A	1011	70.5	5.9	374	14	US-10-060-902-30	Sequence 30, Appl
939	71.5	6.0	538	15	US-10-424-599-248196	Sequence 248196,	1012	70.5	5.9	374	14	US-10-354-247-30	Sequence 30, Appl
940	71.5	6.0	565	14	US-10-176-847-100	Sequence 100, App	1013	70.5	5.9	388	14	US-10-060-902-16	Sequence 16, Appl
941	71.5	6.0	568	9	US-09-843-856-2	Sequence 2, Appl	1014	70.5	5.9	388	14	US-10-354-247-16	Sequence 16, Appl
942	71.5	6.0	603	15	US-10-282-122A-44316	Sequence 44316, A	1015	70.5	5.9	388	14	US-10-060-902-22	Sequence 22, Appl
943	71.5	6.0	689	10	US-09-371-347-48	Sequence 48, Appl	1016	70.5	5.9	390	14	US-10-060-902-24	Sequence 24, Appl
944	71.5	6.0	697	10	US-09-371-347-46	Sequence 46, Appl	1017	70.5	5.9	390	14	US-10-060-902-22	Sequence 22, Appl
945	71.5	6.0	698	10	US-09-371-347-2	Sequence 2, Appl	1018	70.5	5.9	390	14	US-10-354-247-24	Sequence 24, Appl
946	71.5	6.0	698	10	US-09-371-347-21	Sequence 21, Appl	1019	70.5	5.9	393	14	US-10-060-902-28	Sequence 28, Appl
947	71.5	6.0	698	10	US-09-371-347-42	Sequence 42, Appl	1020	70.5	5.9	393	14	US-10-060-902-36	Sequence 36, Appl
948	71.5	6.0	698	10	US-09-371-347-44	Sequence 44, Appl	1021	70.5	5.9	393	14	US-10-354-247-28	Sequence 28, Appl
949	71.5	6.0	890	13	US-10-060-425-2	Sequence 2, Appl	1022	70.5	5.9	393	14	US-10-354-247-18	Sequence 18, Appl
950	71.5	6.0	2560	15	US-10-276-774-1774	Sequence 1774, Ap	1023	70.5	5.9	402	14	US-10-225-567A-234	Sequence 234, App
951	71.5	6.0	2923	9	US-09-788-711A-4	Sequence 4, Appl	1024	70.5	5.9	402	14	US-10-060-902-34	Sequence 34, Appl
952	71.5	6.0	2923	10	US-09-916-849A-3	Sequence 3, Appl	1025	70.5	5.9	402	14	US-10-354-247-34	Sequence 34, Appl
953	71.5	6.0	2923	14	US-10-225-567A-524	Sequence 524, App	1026	70.5	5.9	407	14	US-10-060-902-18	Sequence 18, Appl
954	71.5	6.0	2923	14	US-10-174-677-29	Sequence 29, Appl	1027	70.5	5.9	407	14	US-10-354-247-18	Sequence 18, Appl
955	71.5	6.0	2923	14	US-10-120-801-53	Sequence 53, Appl	1028	70.5	5.9	421	17	US-10-425-115-257457	Sequence 257457,
956	71.5	6.0	2923	14	US-10-292-798-932	Sequence 932, App	1029	70.5	5.9	425	14	US-10-060-902-26	Sequence 26, Appl
957	71.5	6.0	2923	15	US-10-038-854-70	Sequence 70, Appl	1030	70.5	5.9	425	14	US-10-354-247-26	Sequence 26, Appl
958	71.5	6.0	2936	15	US-10-311-623-9	Sequence 9, Appl	1031	70.5	5.9	433	14	US-10-060-902-20	Sequence 20, Appl
959	71.5	6.0	2956	9	US-09-788-711A-2	Sequence 2, Appl	1032	70.5	5.9	433	14	US-10-354-247-20	Sequence 20, Appl
960	71	5.9	117	15	US-10-424-599-275463	Sequence 275463,	1033	70.5	5.9	480	9	US-09-895-913A-92	Sequence 92, Appl
961	71	5.9	240	15	US-10-262-839-72	Sequence 72, Appl	1034	70.5	5.9	494	15	US-10-425-114-65620	Sequence 65620, A
962	71	5.9	295	17	US-10-474-792-346	Sequence 346, App	1035	70.5	5.9	521	15	US-10-282-122A-58397	Sequence 58397, A
963	71	5.9	309	15	US-10-425-114-36801	Sequence 36801, A	1036	70.5	5.9	539	13	US-10-051-902-26	Sequence 26, Appl
964	71	5.9	310	17	US-10-425-115-238819	Sequence 238819,	1037	70.5	5.9	539	13	US-10-051-909-26	Sequence 26, Appl
965	71	5.9	333	17	US-10-425-115-238870	Sequence 238870,	1038	70.5	5.9	548	15	US-10-282-122A-55342	Sequence 55342, A
966	71	5.9	364	15	US-10-425-114-63895	Sequence 63895, A	1039	70.5	5.9	556	14	US-10-369-493-5442	Sequence 5442, Ap
967	71	5.9	438	16	US-10-437-963-181098	Sequence 181098,	1040	70.5	5.9	599	10	US-09-845-908-11	Sequence 11, Appl
968	71	5.9	444	15	US-10-287-226-370	Sequence 370, App	1041	70.5	5.9	717	9	US-09-925-300-1299	Sequence 37, Appl
969	71	5.9	444	15	US-10-287-226-372	Sequence 372, App	1042	70.5	5.9	740	16	US-10-051-909-37	Sequence 37, Appl
970	71	5.9	457	15	US-10-282-122A-47836	Sequence 47836, A	1043	70.5	5.9	740	16	US-10-437-963-195955	Sequence 195955,
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972	71	5.9	470	14	US-10-176-255-25	Sequence 25, Appl	1045	70.5	5.9	1026	14	US-10-032-585-7591	Sequence 7591, Ap

1046	70.5	5.9	1163	15	US-10-336-472-4	Sequence 4, Appli	1119	69.5	5.8	1704	16	US-10-408-765A-2220	Sequence 2230, Ap
1047	70.5	5.9	1781	9	US-09-738-877-3	Sequence 3, Appli	1120	69.5	5.8	1704	16	US-10-648-593-213	Sequence 212, App
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1053	70	5.9	311	10	US-09-908-006A-41	Sequence 41, Appl	1126	69	5.8	281	14	US-10-156-761-14073	Sequence 14073, A
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1055	70	5.9	333	14	US-10-251-385-16	Sequence 16, Appl	1128	69	5.8	301	17	US-10-425-115-328865	Sequence 328865,
1056	70	5.9	333	14	US-10-251-385-172	Sequence 172, App	1129	69	5.8	301	17	US-10-739-930-7363	Sequence 7363, Ap
1057	70	5.9	333	14	US-10-225-567A-279	Sequence 279, App	1130	69	5.8	306	17	US-10-787-098-9	Sequence 9, Appli
1058	70	5.9	333	15	US-10-433-561-32	Sequence 32, Appl	1131	69	5.8	368	15	US-10-424-599-184014	Sequence 184014,
1059	70	5.9	333	16	US-10-477-726-4	Sequence 4, Appli	1132	69	5.8	370	9	US-09-799-955-5	Sequence 5, Appli
1060	70	5.9	333	17	US-10-480-739A-84	Sequence 84, Appl	1133	69	5.8	370	13	US-10-044-592-12	Sequence 12, Appl
1061	70	5.9	333	16	US-10-723-860-2738	Sequence 2738, Ap	1134	69	5.8	370	13	US-10-044-592-74	Sequence 74, Appl
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1064	70	5.9	388	15	US-10-334-360-13	Sequence 13, Appl	1137	69	5.8	370	17	US-10-787-098-8	Sequence 8, Appli
1065	70	5.9	399	14	US-10-094-749-1978	Sequence 1978, Ap	1138	69	5.8	380	16	US-10-611-210-11	Sequence 11, Appl
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1070	70	5.9	602	15	US-10-282-122A-46186	Sequence 46186, A	1143	69	5.8	434	15	US-10-424-599-283401	Sequence 283401,
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1082	69.5	5.8	296	14	US-10-402-842-24	Sequence 24, Appl	1155	69	5.8	163	16	US-10-437-963-189159	Sequence 189159
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1084	69.5	5.8	308	9	US-09-886-055-453	Sequence 453, App	1157	69	5.8	5217	16	US-10-668-767-8	Sequence 8, Appli
1085	69.5	5.8	308	14	US-09-804-291-453	Sequence 453, App	1158	68.5	5.7	169	17	US-10-425-115-368046	Sequence 368046,
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1105	69.5	5.8	568	15	US-10-264-237-2041	Sequence 2041, Ap	1178	68.5	5.7	444	9	US-09-853-386-132	Sequence 136, App
1106	69.5	5.8	573	14	US-10-104-047-3669	Sequence 3669, Ap	1179	68.5	5.7	444	9	US-09-853-386-136	Sequence 15, Appl
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1110	69.5	5.8	663	14	US-10-394-136-2	Sequence 2, Appli	1183	68.5	5.7	447	14	US-10-293-798-708	Sequence 22, Appl
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1112	69.5	5.8	764	15	US-10-389-566-371	Sequence 371, App	1185	68.5	5.7	468	14	US-09-826-509-553	Sequence 638, App
1113	69.5	5.8	801	15	US-10-282-122A-71745	Sequence 71745, A	1186	68.5	5.7	468	14	US-10-292-798-638	Sequence 26, Appl
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1117	69.5	5.8	1704	14	US-10-336-219-120	Sequence 120, App	1190	68.5	5.7	488	10	US-09-992-238-8	Sequence 6813, Ap
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1193	68.5	5.7	481	17	US-10-425-115-261975	Sequence 261975, A	1266	68	5.7	355	9	US-09-886-319A-14	Sequence 14, Appl
1194	68.5	5.7	496	15	US-10-425-118-42719	Sequence 42719, A	1267	68	5.7	355	10	US-09-893-512-11	Sequence 11, Appl
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1197	68.5	5.7	525	13	US-10-044-723-3	Sequence 3, Appli	1270	68	5.7	355	14	US-10-245-850-2	Sequence 2, Appli
1198	68.5	5.7	525	14	US-10-225-567A-231	Sequence 231, App	1271	68	5.7	355	14	US-10-376-564-14	Sequence 14, Appl
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1202	68.5	5.7	548	10	US-09-882-171-469	Sequence 469, App	1275	68	5.7	355	16	US-10-754-071-13	Sequence 13, Appl
1203	68.5	5.7	548	14	US-10-164-861-469	Sequence 469, App	1276	68	5.7	355	16	US-10-755-889-582	Sequence 582, App
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1206	68.5	5.7	553	9	US-09-935-371-29	Sequence 29, Appl	1279	68	5.7	355	17	US-10-723-860-4344	Sequence 4344, Ap
1207	68.5	5.7	553	9	US-09-935-371-29	Sequence 29, Appl	1280	68	5.7	355	17	US-10-370-715B-180	Sequence 180, App
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1209	68.5	5.7	588	15	US-10-276-774-2075	Sequence 2075, Ap	1282	68	5.7	355	17	US-10-832-985-1	Sequence 1, Appli
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Search completed: January 24, 2005, 16:04:40
Job time : 173 secs

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OM protein - protein search, using sw model

Run on: January 24, 2005, 16:00:10 ; Search time 40 Seconds
(without alignments)
387.960 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	79.5	6.7	406	4	US-09-171-699-4
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6	79.5	6.7	723	4	US-09-976-594-503
7	78.5	6.6	221	4	US-09-270-767-41033
8	78.5	6.6	221	4	US-09-270-767-56249
9	78	6.5	228	4	US-09-248-796A-20444
10	78	6.5	251	4	US-09-270-767-43373
11	78	6.5	355	4	US-08-833-752-9
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15	77	6.4	353	3	US-09-479-195-2
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105	71	5.9	470	3	US-09-292-069A-25	Sequence 25, Appl	178	69.5	5.8	453	4	US-09-583-110-3842	Sequence 3842, Ap
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107	71	5.9	470	4	US-09-292-072-25	Sequence 25, Appl	180	69.5	5.8	557	4	US-10-327-189-4	Sequence 4, Appl
108	71	5.9	470	1	US-07-817-920-8	Sequence 8, Appl	181	69.5	5.8	557	4	US-09-521-195B-3	Sequence 3, Appl
109	71	5.9	471	1	US-08-370-542-7	Sequence 7, Appl	182	69.5	5.8	557	4	US-09-798-743-1	Sequence 1, Appl
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111	71	5.9	471	1	US-08-216-594-8	Sequence 8, Appl	184	69.5	5.8	564	4	US-09-489-039A-9425	Sequence 9425, Ap
112	71	5.9	471	1	US-08-542-358-7	Sequence 7, Appl	185	69.5	5.8	599	1	US-08-301-722A-5	Sequence 5, Appl
113	71	5.9	471	2	US-08-244-434-2	Sequence 2, Appl	186	69.5	5.8	660	3	US-09-134-001C-5039	Sequence 5039, Ap
114	71	5.9	471	3	US-09-018-351-7	Sequence 7, Appl	187	69.5	5.8	663	3	US-08-959-004-5	Sequence 5, Appl
115	71	5.9	471	3	US-09-032-742-8	Sequence 8, Appl	188	69.5	5.8	877	4	US-09-165-396-5	Sequence 5, Appl
116	71	5.9	471	3	US-09-145-864-2	Sequence 2, Appl	189	69.5	5.8	1028	4	US-09-328-352-5749	Sequence 5749, Ap
117	71	5.9	471	4	US-09-170-496D-122	Sequence 122, App	190	69.5	5.8	1684	3	US-08-665-259-25	Sequence 25, Appl
118	71	5.9	471	4	US-09-170-496D-228	Sequence 228, App	191	69.5	5.8	1684	3	US-08-762-500-25	Sequence 25, Appl
119	71	5.9	471	4	US-10-092-138A-28	Sequence 28, Appl	192	69.5	5.8	1704	3	US-08-762-500-75	Sequence 75, Appl
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122	71	5.9	2296	3	US-08-980-357-27	Sequence 27, Appl	195	69	5.8	340	4	US-09-248-796A-15237	Sequence 15237, A
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124	70.5	5.9	237	4	US-09-328-352-7074	Sequence 7074, Ap	197	69	5.8	370	3	US-08-513-974B-323	Sequence 223, App
125	70.5	5.9	365	3	US-08-155-005A-8	Sequence 8, Appl	198	69	5.8	370	3	US-09-172-353-5	Sequence 5, Appl
126	70.5	5.9	365	3	US-09-363-783-8	Sequence 8, Appl	199	69	5.8	370	3	US-08-776-971-21	Sequence 21, Appl
127	70.5	5.9	365	4	US-09-661-758A-8	Sequence 8, Appl	200	69	5.8	370	3	US-08-776-971-104	Sequence 104, App
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142	70.5	5.9	539	1	US-07-879-617A-10	Sequence 10, Appl	215	68.5	5.7	199	3	US-09-019-793A-36	Sequence 36, Appl
143	70.5	5.9	539	1	US-08-295-814B-11	Sequence 11, Appl	216	68.5	5.7	200	4	US-09-601-326-36	Sequence 36, Appl
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147	70.5	5.9	539	3	US-09-343-361-11	Sequence 11, Appl	220	68.5	5.7	377	3	US-09-161-994A-12	Sequence 12, Appl
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149	70.5	5.9	1027	2	US-08-551-437-2	Sequence 2, Appl	222	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appl
150	70.5	5.9	1027	3	US-09-004-225-2	Sequence 2, Appl	223	68.5	5.7	383	4	US-08-760-936-4	Sequence 4, Appl
151	70.5	5.9	1027	3	US-09-084-346-2	Sequence 2, Appl	224	68.5	5.7	383	4	US-09-225-024-4	Sequence 4, Appl
152	70.5	5.9	1027	3	US-09-104-704-2	Sequence 4, Appl	225	68.5	5.7	417	4	US-09-134-000C-5002	Sequence 5002, Ap
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154	70.5	5.9	1780	3	US-08-994-570-5	Sequence 5, Appl	227	68.5	5.7	437	4	US-09-328-352-5102	Sequence 5102, Ap
155	70.5	5.9	1781	4	US-09-961-403-13	Sequence 13, Appl	228	68.5	5.7	444	3	US-08-482-746-15	Sequence 15, Appl
156	70	5.9	142	4	US-09-248-796A-27134	Sequence 27134, A	229	68.5	5.7	444	4	US-09-580-734-15	Sequence 15, Appl
157	70	5.9	153	2	US-08-896-365-9	Sequence 9, Appl	230	68.5	5.7	444	4	US-08-374-009-15	Sequence 15, Appl
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160	70	5.9	307	4	US-09-583-110-5003	Sequence 5003, Ap	233	68.5	5.7	448	2	US-08-811-897A-22	Sequence 22, Appl
161	70	5.9	333	1	US-08-148-215A-4	Sequence 4, Appl	234	68.5	5.7	448	2	US-08-855-213-22	Sequence 22, Appl
162	70	5.9	333	4	US-09-170-496D-16	Sequence 16, Appl	235	68.5	5.7	468	3	US-09-201-474-22	Sequence 22, Appl
163	70	5.9	333	4	US-09-170-496D-172	Sequence 172, App	236	68.5	5.7	468	4	US-09-631-603-19	Sequence 19, Appl
164	70	5.9	338	4	US-09-248-796A-17918	Sequence 17918, A	237	68.5	5.7	475	2	US-08-811-897A-26	Sequence 26, Appl
165	70	5.9	361	4	US-09-270-767-40072	Sequence 40072, A	238	68.5	5.7	475	2	US-08-855-213-26	Sequence 26, Appl
166	70	5.9	361	4	US-09-270-767-55288	Sequence 55288, A	239	68.5	5.7	475	3	US-09-201-474-26	Sequence 26, Appl
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168	70	5.9	412	4	US-09-248-796A-22404	Sequence 22404, A	241	68.5	5.7	476	2	US-08-855-213-28	Sequence 28, Appl
169	70	5.9	425	4	US-09-107-532A-6574	Sequence 6574, Ap	242	68.5	5.7	476	2	US-08-855-213-24	Sequence 24, Appl
170	70	5.9	470	4	US-09-328-352-5397	Sequence 5397, Ap	243	68.5	5.7	476	2	US-08-855-213-28	Sequence 28, Appl
171	70	5.9	471	3	US-09-328-314-17	Sequence 17, Appl	244	68.5	5.7	476	3	US-09-201-474-24	Sequence 24, Appl
172	70	5.9	767	4	US-09-540-236-2346	Sequence 2346, Ap	245	68.5	5.7	476	3	US-09-201-474-28	Sequence 28, Appl
173	69.5	5.8	198	4	US-09-328-352-4951	Sequence 4951, Ap	246	68.5	5.7	525	2	US-08-811-897A-23	Sequence 23, Appl

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248	68.5	5.7	525	3	US-09-201-474-23	Sequence 23, Appl	321	68	5.7	2620	2	US-08-904-686A-32	Sequence 32, Appl
249	68.5	5.7	548	4	US-09-149-476-469	Sequence 469, Appl	322	68	5.7	2620	3	US-09-315-850-32	Sequence 32, Appl
250	68.5	5.7	552	2	US-08-811-897A-27	Sequence 27, Appl	323	68	5.7	2621	1	US-08-324-977-36	Sequence 36, Appl
251	68.5	5.7	552	2	US-08-855-213-27	Sequence 27, Appl	324	68	5.7	2621	1	US-08-384-616-36	Sequence 36, Appl
252	68.5	5.7	552	3	US-09-201-474-27	Sequence 27, Appl	325	68	5.7	2621	2	US-08-904-686A-36	Sequence 36, Appl
253	68.5	5.7	553	2	US-08-811-897A-25	Sequence 25, Appl	326	68	5.7	2621	3	US-09-315-850-36	Sequence 36, Appl
254	68.5	5.7	553	2	US-08-811-897A-29	Sequence 29, Appl	327	68	5.7	3010	1	US-08-324-977-2	Sequence 2, Appl
255	68.5	5.7	553	2	US-08-855-213-25	Sequence 25, Appl	328	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
256	68.5	5.7	553	2	US-08-855-213-29	Sequence 29, Appl	329	68	5.7	3010	2	US-08-384-616-2	Sequence 2, Appl
257	68.5	5.7	553	3	US-09-201-474-25	Sequence 25, Appl	330	68	5.7	3010	2	US-08-384-616-14	Sequence 14, Appl
258	68.5	5.7	553	3	US-09-201-474-29	Sequence 29, Appl	331	68	5.7	3010	2	US-08-904-686A-2	Sequence 2, Appl
259	68.5	5.7	660	4	US-09-252-991A-29885	Sequence 29885, A	332	68	5.7	3010	2	US-08-904-686A-14	Sequence 14, Appl
260	68.5	5.7	738	4	US-09-107-532A-5096	Sequence 5096, Ap	333	68	5.7	3010	3	US-09-315-850-2	Sequence 2, Appl
261	68.5	5.7	1296	4	US-09-462-136-9	Sequence 9, Appl	334	68	5.7	3010	3	US-09-315-850-14	Sequence 14, Appl
262	68	5.7	188	4	US-09-270-767-36930	Sequence 36930, A	335	67.5	5.6	210	4	US-09-248-796A-20156	Sequence 20156, A
263	68	5.7	188	4	US-09-270-767-52147	Sequence 52147, A	336	67.5	5.6	253	4	US-09-540-236-3093	Sequence 3093, Ap
264	68	5.7	258	3	US-09-053-197A-7	Sequence 7, Appl	337	67.5	5.6	306	4	US-09-252-991A-32161	Sequence 32161, A
265	68	5.7	258	3	US-09-085-761A-7	Sequence 7, Appl	338	67.5	5.6	350	2	US-08-966-116-16	Sequence 16, Appl
266	68	5.7	309	4	US-09-328-352-6344	Sequence 6344, Ap	339	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
267	68	5.7	346	4	US-09-585-876-2	Sequence 2, Appl	340	67.5	5.6	457	4	US-09-543-681A-6044	Sequence 6044, Ap
268	68	5.7	355	1	US-08-012-988A-2	Sequence 2, Appl	341	67.5	5.6	459	4	US-09-694-519-3	Sequence 3, Appl
269	68	5.7	355	1	US-08-450-393A-5	Sequence 5, Appl	342	67.5	5.6	459	4	US-09-694-519-8	Sequence 8, Appl
270	68	5.7	355	3	US-08-446-669-5	Sequence 5, Appl	343	67.5	5.6	524	4	US-09-198-452A-369	Sequence 369, App
271	68	5.7	355	3	US-09-239-938-1	Sequence 1, Appl	344	67.5	5.6	586	4	US-09-252-991A-17104	Sequence 17104, A
272	68	5.7	355	4	US-09-886-319A-14	Sequence 14, Appl	345	67.5	5.6	865	4	US-09-452-991A-18683	Sequence 18683, A
273	68	5.7	355	4	US-10-039-659A-13	Sequence 13, Appl	346	67.5	5.6	1324	2	US-08-811-897A-56	Sequence 56, Appl
274	68	5.7	355	4	US-09-961-068-1	Sequence 1, Appl	347	67.5	5.6	1324	3	US-09-201-474-56	Sequence 56, Appl
275	68	5.7	355	4	US-09-625-573-5	Sequence 5, Appl	348	67.5	5.6	1411	4	US-09-538-092-413	Sequence 413, App
276	68	5.7	355	4	US-09-960-547-1	Sequence 1, Appl	349	67.5	5.6	2318	3	US-09-091-219-24	Sequence 24, Appl
277	68	5.7	355	5	PCT-US95-00476-5	Sequence 5, Appl	350	67.5	5.6	2318	4	US-09-660-541-24	Sequence 24, Appl
278	68	5.7	373	4	US-09-107-532A-7048	Sequence 7048, Ap	351	67	5.6	153	4	US-09-198-452A-329	Sequence 329, App
279	68	5.7	414	4	US-09-489-039A-10869	Sequence 10869, A	352	67	5.6	159	4	US-09-134-000C-4969	Sequence 4969, Ap
280	68	5.7	426	4	US-09-486-192-2	Sequence 2, Appl	353	67	5.6	199	3	US-08-478-316-32	Sequence 32, Appl
281	68	5.7	471	3	US-08-492-459-14	Sequence 14, Appl	354	67	5.6	199	3	US-09-019-793A-32	Sequence 32, Appl
282	68	5.7	471	3	US-08-423-752-14	Sequence 14, Appl	355	67	5.6	200	1	US-08-131-625B-11	Sequence 11, Appl
283	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	356	67	5.6	200	4	US-08-301-435-15	Sequence 15, Appl
284	68	5.7	471	3	US-08-716-873-28	Sequence 28, Appl	357	67	5.6	200	4	US-09-601-326-32	Sequence 32, Appl
285	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	358	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl
286	68	5.7	471	3	US-09-368-431-28	Sequence 28, Appl	359	67	5.6	207	4	US-08-811-519-26	Sequence 26, Appl
287	68	5.7	471	3	US-09-414-006-14	Sequence 14, Appl	360	67	5.6	272	4	US-09-270-767-37728	Sequence 37728, A
288	68	5.7	471	4	US-09-447-223-14	Sequence 14, Appl	361	67	5.6	272	4	US-09-270-767-52945	Sequence 52945, A
289	68	5.7	471	4	US-09-951-217-8	Sequence 8, Appl	362	67	5.6	282	4	US-09-270-767-50952	Sequence 50952, A
290	68	5.7	471	4	US-09-951-217-28	Sequence 28, Appl	363	67	5.6	282	4	US-09-270-767-50952	Sequence 50952, A
291	68	5.7	471	4	US-09-792-024-88	Sequence 88, Appl	364	67	5.6	282	4	US-09-372-422A-38	Sequence 38, Appl
292	68	5.7	472	3	US-08-492-459-22	Sequence 22, Appl	365	67	5.6	295	3	US-09-107-532A-4523	Sequence 4523, Ap
293	68	5.7	472	3	US-08-423-752-22	Sequence 22, Appl	366	67	5.6	464	4	US-09-248-796A-18187	Sequence 18187, A
294	68	5.7	472	3	US-08-716-873-36	Sequence 36, Appl	367	67	5.6	479	4	US-09-543-681A-6605	Sequence 6605, Ap
295	68	5.7	472	3	US-09-368-431-36	Sequence 36, Appl	368	67	5.6	480	1	US-08-440-103-18	Sequence 18, Appl
296	68	5.7	472	3	US-09-414-006-22	Sequence 22, Appl	369	67	5.6	480	1	US-08-440-542-18	Sequence 18, Appl
297	68	5.7	472	4	US-09-447-223-22	Sequence 22, Appl	370	67	5.6	480	1	US-08-231-368-18	Sequence 18, Appl
298	68	5.7	472	4	US-09-951-217-36	Sequence 36, Appl	371	67	5.6	480	1	US-08-440-210-18	Sequence 18, Appl
299	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl	372	67	5.6	480	3	US-09-046-604-18	Sequence 18, Appl
300	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl	373	67	5.6	733	4	US-09-489-039A-7885	Sequence 7885, Ap
301	68	5.7	480	1	US-08-231-368-22	Sequence 22, Appl	374	67	5.6	978	4	US-09-585-858-20	Sequence 20, Appl
302	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl	375	67	5.6	1093	4	US-09-248-796A-17108	Sequence 17108, A
303	68	5.7	480	3	US-09-046-604-22	Sequence 22, Appl	376	67	5.6	1174	1	US-08-040-751-3	Sequence 3, Appl
304	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appl	377	67	5.6	1174	1	US-08-291-368-2	Sequence 2, Appl
305	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appl	378	67	5.6	1174	2	US-08-962-190-2	Sequence 2, Appl
306	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appl	379	67	5.6	1174	5	PCT-US95-10310-2	Sequence 2, Appl
307	68	5.7	503	1	US-08-483-094-4	Sequence 4, Appl	380	67	5.6	1174	6	5164180-4	Patent No. 5164180
308	68	5.7	727	1	US-08-424-424B-2	Sequence 2, Appl	381	67	5.6	1242	4	US-08-680-326-33	Sequence 33, Appl
309	68	5.7	727	5	PCT-US94-05363A-2	Sequence 2, Appl	382	67	5.6	1242	4	US-09-904-065-12	Sequence 12, Appl
310	68	5.7	859	3	US-09-538-092-206	Sequence 206, App	383	67	5.6	1242	4	US-09-904-065-13	Sequence 13, Appl
311	68	5.7	908	3	US-08-823-110-1	Sequence 1, Appl	384	67	5.6	3010	4	US-09-539-601-3	Sequence 3, Appl
312	68	5.7	908	3	US-08-604-298-1	Sequence 1, Appl	385	67	5.6	3010	4	US-09-539-601-21	Sequence 21, Appl
313	68	5.7	968	3	US-08-651-999A-7	Sequence 7, Appl	386	67	5.6	3010	4	US-09-539-601-27	Sequence 27, Appl
314	68	5.7	968	3	US-09-385-752-7	Sequence 7, Appl	387	67	5.6	3010	4	US-09-539-601-33	Sequence 33, Appl
315	68	5.7	2013	1	US-08-324-977-12	Sequence 12, Appl	388	67	5.6	3287	2	US-08-477-451-7	Sequence 7, Appl
316	68	5.7	2013	2	US-08-384-616-12	Sequence 12, Appl	389	66.5	5.6	197	4	US-09-134-000C-4925	Sequence 4925, Ap
317	68	5.7	2013	2	US-08-904-686A-12	Sequence 12, Appl	390	66.5	5.6	200	3	US-08-686-968C-9	Sequence 9, Appl
318	68	5.7	2013	3	US-09-315-850-12	Sequence 12, Appl	391	66.5	5.6	243	4	US-09-328-352-7321	Sequence 7321, Ap
319	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl	392	66.5	5.6	288	2	US-08-466-103A-6	Sequence 6, Appl

393	66.5	289	4	US-09-248-796A-17919	Sequence 17919, A	466	66	5.5	370	4	US-09-576-290-140	Sequence 140, Appl
394	66.5	293	4	US-09-248-796A-18278	Sequence 18278, A	467	66	5.5	381	2	US-08-845-566-3	Sequence 3, Appl
395	66.5	341	4	US-09-248-796A-18985	Sequence 18985, A	468	66	5.5	381	2	US-08-467-948A-28	Sequence 28, Appl
396	66.5	345	3	US-09-291-922-14	Sequence 14, Appl	469	66	5.5	381	3	US-08-852-824-18	Sequence 18, Appl
397	66.5	359	4	US-09-828-523A-14	Sequence 14, Appl	470	66	5.5	381	3	US-08-467-947A-28	Sequence 28, Appl
398	66.5	370	4	US-09-828-523A-74	Sequence 74, Appl	471	66	5.5	381	4	US-09-731-030A-17	Sequence 17, Appl
399	66.5	389	4	US-09-134-000C-3706	Sequence 3706, Ap	472	66	5.5	381	5	PCT-US96-10618-4	Sequence 4, Appl
400	66.5	413	4	US-09-328-352-5589	Sequence 5589, Ap	473	66	5.5	405	4	US-09-799-378-38	Sequence 38, Appl
401	66.5	430	4	US-09-583-110-4230	Sequence 4230, Ap	474	66	5.5	412	4	US-10-138-701-59	Sequence 59, Appl
402	66.5	454	3	US-08-444-818-73	Sequence 73, Appl	475	66	5.5	433	4	US-09-134-000C-6536	Sequence 6536, Ap
403	66.5	468	4	US-09-248-796A-27314	Sequence 27314, A	476	66	5.5	447	4	US-09-825-923-2	Sequence 2, Appl
404	66.5	480	1	US-08-440-103-14	Sequence 14, Appl	477	66	5.5	450	4	US-09-825-923-4	Sequence 4, Appl
405	66.5	480	1	US-08-440-542-14	Sequence 14, Appl	478	66	5.5	582	4	US-09-721-870-179	Sequence 179, App
406	66.5	480	1	US-08-231-368-14	Sequence 14, Appl	479	66	5.5	583	4	US-09-270-767-38131	Sequence 38131, A
407	66.5	480	1	US-08-440-210-14	Sequence 14, Appl	480	66	5.5	583	4	US-09-270-767-53348	Sequence 53348, A
408	66.5	480	1	US-09-046-604-14	Sequence 14, Appl	481	66	5.5	1250	3	US-08-938-291A-9	Sequence 9, Appl
409	66.5	537	4	US-09-489-039A-14149	Sequence 14149, A	482	66	5.5	1250	3	US-09-589-619-9	Sequence 9, Appl
410	66.5	550	2	US-08-121-057-4	Sequence 4, Appl	483	65.5	5.5	145	4	US-09-134-000C-3453	Sequence 3453, Ap
411	66.5	550	2	US-08-509-187D-4	Sequence 4, Appl	484	65.5	5.5	155	4	US-09-134-000C-3721	Sequence 3721, Ap
412	66.5	550	2	US-09-121-396-4	Sequence 4, Appl	485	65.5	5.5	166	3	US-09-134-001C-4279	Sequence 4279, Ap
413	66.5	550	5	PCT-US93-09704A-4	Sequence 4, Appl	486	65.5	5.5	210	4	US-09-538-092-121	Sequence 121, App
414	66.5	557	4	US-09-328-352-4917	Sequence 15455, A	487	65.5	5.5	291	4	US-09-252-991A-32938	Sequence 32938, A
415	66.5	627	4	US-08-824-057-3	Sequence 4917, Ap	488	65.5	5.5	356	4	US-09-172-353-6	Sequence 6286, Ap
416	66.5	663	3	US-09-415-582-3	Sequence 3, Appl	489	65.5	5.5	369	3	US-09-799-955-6	Sequence 6, Appl
417	66.5	663	3	US-08-633-596-4	Sequence 3, Appl	490	65.5	5.5	369	4	US-09-170-436D-26	Sequence 26, Appl
418	66.5	738	3	US-08-867-611-35	Sequence 35, Appl	491	65.5	5.5	369	4	US-09-170-436D-178	Sequence 178, App
419	66.5	738	3	US-09-690-359-35	Sequence 35, Appl	492	65.5	5.5	407	4	US-09-252-991A-21511	Sequence 21511, A
420	66.5	738	5	PCT-US92-06965A-5	Sequence 35, Appl	493	65.5	5.5	459	4	US-09-694-519-4	Sequence 4, Appl
421	66.5	801	4	US-09-710-279-90	Sequence 90, Appl	494	65.5	5.5	468	4	US-09-252-991A-17314	Sequence 17314, A
422	66.5	802	3	US-09-134-001C-3741	Sequence 3741, Ap	495	65.5	5.5	468	4	US-09-583-110-4658	Sequence 4658, Ap
423	66.5	802	3	US-09-134-000C-5653	Sequence 5653, Ap	496	65.5	5.5	487	4	US-09-107-532A-6945	Sequence 6945, Ap
424	66.5	977	4	US-08-732-024-98	Sequence 98, Appl	497	65.5	5.5	492	4	US-09-248-796A-15726	Sequence 15726, A
425	66.5	1897	4	US-08-444-818-66	Sequence 66, Appl	498	65.5	5.5	565	4	US-09-342-647-2	Sequence 2, Appl
426	66.5	2261	3	US-08-466-975A-23	Sequence 23, Appl	499	65.5	5.5	630	3	US-09-657-960-3	Sequence 3, Appl
427	66.5	2894	2	US-08-391-671A-23	Sequence 23, Appl	500	65.5	5.5	718	4	US-08-092-817-4	Sequence 4, Appl
428	66.5	2894	2	US-08-467-902A-23	Sequence 23, Appl	501	65.5	5.5	860	1	US-08-485-128-8	Sequence 8, Appl
429	66.5	2894	3	US-09-275-265-23	Sequence 23, Appl	502	65.5	5.5	860	3	US-09-804-778A-8	Sequence 8, Appl
430	66.5	2894	4	US-09-941-611-23	Sequence 23, Appl	503	65.5	5.5	860	4	US-09-824-637-4	Sequence 4, Appl
431	66.5	2894	2	US-08-443-260-3	Sequence 3, Appl	504	65.5	5.5	860	4	US-09-248-796A-20776	Sequence 20776, A
432	66.5	2955	2	US-08-442-805A-3	Sequence 3, Appl	505	65.5	5.5	959	2	US-08-540-804-12	Sequence 12, Appl
433	66.5	2955	3	US-08-443-900A-3	Sequence 3, Appl	506	65.5	5.5	1226	2	US-08-218-265-12	Sequence 12, Appl
434	66.5	2955	3	US-08-444-818-124	Sequence 124, App	507	65.5	5.5	1226	2	US-08-521-872-12	Sequence 12, Appl
435	66.5	2955	3	US-08-249-843-3	Sequence 138, App	508	65.5	5.5	1226	3	US-08-590-399-12	Sequence 12, Appl
436	66.5	2955	3	US-08-444-818-138	Sequence 3, Appl	509	65.5	5.5	1226	3	US-08-470-058-4	Sequence 4, Appl
437	66.5	3010	3	US-09-014-416-3	Sequence 3, Appl	510	65.5	5.5	1410	2	US-09-037-180-4	Sequence 4, Appl
438	66.5	3010	1	US-08-440-103-36	Sequence 36, Appl	511	65.5	5.5	1410	3	US-09-285-310-4	Sequence 4, Appl
439	66.5	3011	1	US-08-440-542-36	Sequence 36, Appl	512	65.5	5.5	1410	3	US-09-107-532A-3813	Sequence 3813, Ap
440	66.5	3011	1	US-07-910-760-10	Sequence 10, Appl	513	65	5.4	126	4	US-10-002-720-46	Sequence 46, Appl
441	66.5	3011	1	US-08-440-519-10	Sequence 10, Appl	514	65	5.4	176	4	US-10-002-720-45	Sequence 45, Appl
442	66.5	3011	1	US-08-231-368-36	Sequence 36, Appl	515	65	5.4	180	4	US-09-126-640-10	Sequence 10, Appl
443	66.5	3011	1	US-08-440-210-36	Sequence 36, Appl	516	65	5.4	181	3	US-09-288-292A-10	Sequence 10, Appl
444	66.5	3011	2	US-08-833-678A-6	Sequence 6, Appl	517	65	5.4	181	3	US-08-826-246-8	Sequence 8, Appl
445	66.5	3011	3	US-08-444-818-177	Sequence 177, App	518	65	5.4	182	3	US-08-944-495-8	Sequence 8, Appl
446	66.5	3011	3	US-09-014-416-5	Sequence 5, Appl	519	65	5.4	182	3	US-08-925-588-8	Sequence 8, Appl
447	66.5	3011	3	US-08-529-169A-6	Sequence 6, Appl	520	65	5.4	182	4	US-09-372-044-8	Sequence 8, Appl
448	66.5	3011	3	US-09-388-874-2	Sequence 2, Appl	521	65	5.4	182	4	US-08-825-486-8	Sequence 8, Appl
449	66.5	3011	3	US-09-046-604-36	Sequence 36, Appl	522	65	5.4	182	4	US-08-826-248-8	Sequence 8, Appl
450	66.5	3011	3	US-08-440-549-10	Sequence 10, Appl	523	65	5.4	182	4	US-09-328-352-6034	Sequence 6034, Ap
451	66.5	3011	3	US-08-850-328-1	Sequence 1, Appl	524	65	5.4	223	4	US-10-162-012-9	Sequence 9, Appl
452	66.5	3011	4	US-09-483-799-6	Sequence 6, Appl	525	65	5.4	223	4	US-09-303-456-79	Sequence 79, Appl
453	66.5	3011	5	PCT-US91-02225-10	Sequence 10, Appl	526	65	5.4	272	4	US-09-107-532A-5538	Sequence 5538, Ap
454	66.5	3011	5	US-09-270-767-61535	Sequence 61535, A	527	65	5.4	311	4	US-09-538-092-506	Sequence 506, App
455	66	192	4	US-09-248-796A-15621	Sequence 15621, A	528	65	5.4	322	4	US-09-095-163-2	Sequence 2, Appl
456	66	219	4	US-09-107-532A-5717	Sequence 5717, Ap	529	65	5.4	336	3	US-09-485-648-6	Sequence 6, Appl
457	66	282	3	US-09-134-001C-2917	Sequence 2917, Ap	530	65	5.4	362	3	US-09-503-565-6	Sequence 6, Appl
458	66	282	3	US-09-107-532A-4973	Sequence 4973, Ap	531	65	5.4	362	4	US-09-485-649-6	Sequence 6, Appl
459	66	302	4	US-09-328-352-6692	Sequence 6692, Ap	532	65	5.4	362	4	US-09-799-978-6	Sequence 8, Appl
460	66	316	4	US-09-172-353-7	Sequence 7, Appl	533	65	5.4	375	4	US-09-799-978-6	Sequence 8, Appl
461	66	370	3	US-08-776-971-140	Sequence 140, App	534	65	5.4	401	4	US-08-110-286A-2	Sequence 2, Appl
462	66	370	3	US-08-776-971-140	Sequence 7, Appl	535	65	5.4	415	3	US-08-482-746-2	Sequence 2, Appl
463	66	370	3	US-08-776-971-140	Sequence 7, Appl	536	65	5.4	415	3	US-08-482-746-2	Sequence 2, Appl
464	66	370	3	US-08-776-971-140	Sequence 7, Appl	537	65	5.4	415	3	US-08-482-746-2	Sequence 2, Appl
465	66	370	4	US-09-799-955-7	Sequence 7, Appl	538	65	5.4	415	4	US-09-580-734-2	Sequence 2, Appl

539	65	5.4	415	4	US-08-374-009-2	Sequence 2, Appli	612	64	5.4	284	4	US-09-270-767-37726	Sequence 37726, A
540	65	5.4	415	4	US-09-191-724-2	Sequence 2, Appli	613	64	5.4	284	4	US-09-270-767-52943	Sequence 52943, A
541	65	5.4	415	4	US-09-799-978-2	Sequence 2, Appli	614	64	5.4	285	4	US-09-248-796A-14187	Sequence 14187, A
542	65	5.4	415	4	US-09-799-978-4	Sequence 4, Appli	615	64	5.4	296	3	US-09-100-804-12	Sequence 12, Appl
543	65	5.4	415	4	US-09-799-978-40	Sequence 40, Appli	616	64	5.4	325	4	US-09-107-532A-4900	Sequence 4900, Ap
544	65	5.4	432	4	US-09-710-279-780	Sequence 780, App	617	64	5.4	336	4	US-09-848-294-5	Sequence 5, Appli
545	65	5.4	441	4	US-09-540-236-2016	Sequence 2016, Ap	618	64	5.4	351	3	US-08-688-988-28	Sequence 28, Appl
546	65	5.4	461	2	US-08-672-814D-2	Sequence 2, Appli	619	64	5.4	357	4	US-09-489-039A-10505	Sequence 10505, A
547	65	5.4	461	3	US-09-333-696-2	Sequence 2, Appli	620	64	5.4	363	4	US-09-248-796A-19011	Sequence 19011, A
548	65	5.4	461	4	US-09-282-218A-2	Sequence 2, Appli	621	64	5.4	364	4	US-09-489-039A-12017	Sequence 12017, A
549	65	5.4	463	3	US-08-612-973-46	Sequence 46, Appl	622	64	5.4	387	3	US-09-134-001C-4082	Sequence 4082, Ap
550	65	5.4	463	3	US-08-927-597-46	Sequence 46, Appl	623	64	5.4	411	1	US-08-381-433A-4	Sequence 4, Appli
551	65	5.4	490	3	US-08-612-973-36	Sequence 36, Appl	624	64	5.4	411	3	US-08-981-189B-12	Sequence 12, Appl
552	65	5.4	490	3	US-08-927-597-36	Sequence 36, Appl	625	64	5.4	411	4	US-09-799-978-18	Sequence 18, Appl
553	65	5.4	491	4	US-09-181-339-7	Sequence 7, Appli	626	64	5.4	411	4	US-09-881-401-4	Sequence 4, Appli
554	65	5.4	637	4	US-09-543-681A-5869	Sequence 5869, Ap	627	64	5.4	412	4	US-09-489-039A-8361	Sequence 8361, Ap
555	65	5.4	692	3	US-08-612-973-48	Sequence 48, Appl	628	64	5.4	413	4	US-09-491-577-72	Sequence 72, Appl
556	65	5.4	692	3	US-08-927-597-48	Sequence 48, Appl	629	64	5.4	416	4	US-09-540-236-2393	Sequence 2393, Ap
557	65	5.4	809	3	US-08-612-973-50	Sequence 50, Appl	630	64	5.4	420	4	US-09-583-447A-6	Sequence 6, Appli
558	65	5.4	809	3	US-08-927-597-50	Sequence 50, Appl	631	64	5.4	431	3	US-08-981-189B-13	Sequence 13, Appl
559	65	5.4	1033	4	US-09-328-352-5138	Sequence 5138, Ap	632	64	5.4	431	4	US-09-799-978-20	Sequence 20, Appl
560	64.5	5.4	215	4	US-09-107-532A-3730	Sequence 3730, Ap	633	64	5.4	431	4	US-09-881-401-2	Sequence 2, Appli
561	64.5	5.4	263	1	US-08-565-386-9	Sequence 9, Appli	634	64	5.4	448	4	US-09-252-991A-23910	Sequence 23910, A
562	64.5	5.4	271	4	US-09-328-352-7066	Sequence 7066, Ap	635	64	5.4	469	4	US-09-328-352-4250	Sequence 4250, Ap
563	64.5	5.4	311	4	US-09-252-991A-17395	Sequence 17395, A	636	64	5.4	489	2	US-09-062-890-38	Sequence 38, Appl
564	64.5	5.4	328	4	US-09-489-039A-13216	Sequence 13216, A	637	64	5.4	503	4	US-09-583-447A-2	Sequence 2, Appli
565	64.5	5.4	333	4	US-09-107-532A-4886	Sequence 4886, Ap	638	64	5.4	504	4	US-09-583-447A-4	Sequence 4, Appli
566	64.5	5.4	344	2	US-08-726-575A-2	Sequence 2, Appli	639	64	5.4	534	4	US-09-710-279-920	Sequence 920, App
567	64.5	5.4	349	3	US-09-134-001C-4519	Sequence 4519, Ap	640	64	5.4	555	4	US-09-543-681A-4582	Sequence 4582, Ap
568	64.5	5.4	393	4	US-09-270-767-42317	Sequence 42317, A	641	64	5.4	586	3	US-09-040-725A-1	Sequence 1, Appli
569	64.5	5.4	398	4	US-09-583-110-4666	Sequence 4666, Ap	642	64	5.4	686	4	US-09-134-000C-5066	Sequence 5066, Ap
570	64.5	5.4	407	4	US-09-328-352-5605	Sequence 5605, Ap	643	64	5.4	757	4	US-09-585-858-23	Sequence 23, Appl
571	64.5	5.4	411	2	US-08-336-031-2	Sequence 2, Appli	644	64	5.4	967	1	US-08-188-281B-13	Sequence 13, Appl
572	64.5	5.4	411	2	US-08-902-853-7	Sequence 7, Appli	645	64	5.4	967	5	PCT-US94-07280-13	Sequence 13, Appl
573	64.5	5.4	411	5	PCT-US95-06725-2	Sequence 2, Appli	646	64	5.4	967	5	PCT-US95-01087-13	Sequence 13, Appl
574	64.5	5.4	413	4	US-09-799-978-32	Sequence 32, Appl	647	64	5.4	1116	4	US-09-543-681A-4379	Sequence 4379, Ap
575	64.5	5.4	418	5	PCT-US94-01321-72	Sequence 72, Appl	648	64	5.4	1462	3	US-07-792-600-31	Sequence 31, Appl
576	64.5	5.4	437	3	US-09-353-332-2	Sequence 2, Appli	649	64	5.4	1462	3	US-09-157-021-31	Sequence 31, Appl
577	64.5	5.4	446	1	US-07-781-254A-2	Sequence 2, Appli	650	64	5.4	1462	3	US-09-156-842-31	Sequence 31, Appl
578	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appli	651	64	5.4	1462	4	US-09-591-514-31	Sequence 31, Appl
579	64.5	5.4	447	4	US-09-252-991A-20563	Sequence 20563, A	652	64	5.4	1648	1	US-08-188-281B-12	Sequence 12, Appl
580	64.5	5.4	448	2	US-08-811-897A-18	Sequence 18, Appl	653	64	5.4	1648	5	PCT-US94-07280-12	Sequence 12, Appl
581	64.5	5.4	448	2	US-08-855-213-18	Sequence 18, Appl	654	64	5.4	1648	3	PCT-US95-01087-12	Sequence 12, Appl
582	64.5	5.4	448	3	US-09-201-474-18	Sequence 18, Appl	655	64	5.4	2436	3	US-08-444-818-75	Sequence 75, Appl
583	64.5	5.4	464	4	US-09-107-532A-5509	Sequence 5509, Ap	656	64	5.4	2772	3	US-08-444-818-89	Sequence 89, Appl
584	64.5	5.4	467	2	US-08-811-897A-19	Sequence 19, Appl	657	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appli
585	64.5	5.4	467	2	US-08-855-213-19	Sequence 19, Appl	658	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appli
586	64.5	5.4	467	2	US-09-201-474-19	Sequence 19, Appl	659	64	5.4	3011	2	US-08-710-637-1	Sequence 1, Appli
587	64.5	5.4	476	2	US-08-811-897A-20	Sequence 20, Appl	660	64	5.4	3011	5	PCT-US93-00907-1	Sequence 1, Appli
588	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl	661	64	5.4	3011	5	PCT-US94-07280-1	Sequence 1, Appli
589	64.5	5.4	476	3	US-09-201-474-20	Sequence 20, Appl	662	64	5.4	3011	5	PCT-US95-01087-1	Sequence 1, Appli
590	64.5	5.4	482	4	US-09-107-532A-4512	Sequence 4512, Ap	663	63.5	5.3	118	3	US-09-627-376-17	Sequence 17, Appl
591	64.5	5.4	483	4	US-09-134-000C-4234	Sequence 4234, Ap	664	63.5	5.3	118	3	US-10-047-676B-17	Sequence 17, Appl
592	64.5	5.4	486	3	US-09-231-922-10	Sequence 10, Appl	665	63.5	5.3	124	4	US-09-270-767-34829	Sequence 34829, A
593	64.5	5.4	494	2	US-09-031-392-5	Sequence 5, Appli	666	63.5	5.3	124	4	US-09-270-767-50046	Sequence 50046, A
594	64.5	5.4	494	3	US-09-299-549-5	Sequence 5, Appli	667	63.5	5.3	134	4	US-09-513-999C-6305	Sequence 6305, Ap
595	64.5	5.4	495	3	US-09-610-417-5	Sequence 5, Appli	668	63.5	5.3	209	4	US-09-134-000C-3922	Sequence 3922, Ap
596	64.5	5.4	495	2	US-08-811-897A-21	Sequence 21, Appl	669	63.5	5.3	219	4	US-09-270-767-41489	Sequence 41489, A
597	64.5	5.4	495	2	US-08-855-213-21	Sequence 21, Appl	670	63.5	5.3	253	4	US-09-602-787A-8	Sequence 8, Appli
598	64.5	5.4	495	3	US-09-201-474-21	Sequence 21, Appl	671	63.5	5.3	284	4	US-09-489-039A-9738	Sequence 9738, Ap
599	64.5	5.4	557	4	US-09-521-195B-27	Sequence 27, Appl	672	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl
600	64.5	5.4	557	4	US-09-798-743-3	Sequence 3, Appli	673	63.5	5.3	275	3	PCT-US93-08528-66	Sequence 66, Appl
601	64.5	5.4	570	4	US-09-248-796A-19123	Sequence 19123, A	674	63.5	5.3	279	3	US-09-134-001C-4667	Sequence 4667, Ap
602	64.5	5.4	576	3	US-08-948-564-16	Sequence 16, Appl	675	63.5	5.3	280	1	US-08-781-562-4	Sequence 4, Appli
603	64.5	5.4	747	3	US-09-231-922-2	Sequence 2, Appli	676	63.5	5.3	308	4	US-09-252-991A-16800	Sequence 16800, A
604	64.5	5.4	757	4	US-09-585-858-24	Sequence 24, Appl	677	63.5	5.3	342	3	US-09-116-498-4	Sequence 4, Appli
605	64.5	5.4	795	4	US-09-107-532A-5429	Sequence 5429, Ap	678	63.5	5.3	342	3	US-09-116-498-6	Sequence 6, Appli
606	64.5	5.4	3033	1	US-07-925-695-8	Sequence 8, Appli	679	63.5	5.3	342	3	US-09-852-156-4	Sequence 4, Appli
607	64	5.4	106	4	US-09-270-767-41157	Sequence 41157, A	680	63.5	5.3	342	4	US-09-852-156-6	Sequence 6, Appli
608	64	5.4	106	4	US-09-270-767-56373	Sequence 56373, A	681	63.5	5.3	349	4	US-09-252-991A-24644	Sequence 24644, A
609	64	5.4	168	4	US-09-543-681A-61293	Sequence 6129, Ap	682	63.5	5.3	350	4	US-09-556-002-2	Sequence 2, Appli
610	64	5.4	198	4	US-09-248-796A-17465	Sequence 17465, A	683	63.5	5.3	358	4	US-09-270-767-41449	Sequence 41449, A
611	64	5.4	216	4	US-09-270-767-46297	Sequence 46297, A	684	63.5	5.3	365	4	US-09-933-999A-5	Sequence 5, Appli

685	63.5	5.3	372	1	US-08-202-056-5	Sequence 5, Appli	758	63	5.3	640	4	US-09-252-991A-27542	Sequence 27542, A
686	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appli	759	63	5.3	692	4	US-09-540-236-3150	Sequence 3150, Ap
687	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appli	760	63	5.3	729	3	US-09-291-922-29	Sequence 29, Appl
688	63.5	5.3	372	1	US-08-284-586-6	Sequence 6, Appli	761	63	5.3	795	4	US-09-252-991A-19085	Sequence 19085, A
689	63.5	5.3	372	2	US-08-805-478-6	Sequence 6, Appli	762	63	5.3	822	4	US-08-684-932A-38	Sequence 38, Appl
690	63.5	5.3	372	2	US-08-802-627A-6	Sequence 6, Appli	763	63	5.3	822	4	US-09-618-204B-2	Sequence 2, Appli
691	63.5	5.3	372	2	US-08-801-238-6	Sequence 6, Appli	764	63	5.3	822	4	US-08-469-537A-107	Sequence 107, App
692	63.5	5.3	372	2	US-08-801-228-6	Sequence 6, Appli	765	63	5.3	1802	3	US-09-322-478-18	Sequence 18, Appl
693	63.5	5.3	372	2	US-08-104-296-6	Sequence 6, Appli	766	63	5.3	1802	4	US-09-586-106D-18	Sequence 18, Appl
694	63.5	5.3	372	3	US-08-982-493-8	Sequence 6, Appli	767	62.5	5.2	80	4	US-09-248-796A-26578	Sequence 26578, A
695	63.5	5.3	372	4	US-09-170-496D-66	Sequence 66, Appl	768	62.5	5.2	136	2	US-08-477-451-31	Sequence 31, Appl
696	63.5	5.3	372	4	US-09-170-496D-200	Sequence 200, App	769	62.5	5.2	140	4	US-09-270-767-40416	Sequence 40416, A
697	63.5	5.3	372	4	US-09-248-796A-14491	Sequence 14491, A	770	62.5	5.2	140	4	US-09-270-767-55632	Sequence 55632, A
698	63.5	5.3	379	4	US-09-583-110-2946	Sequence 2946, Ap	771	62.5	5.2	161	3	US-09-413-814-15	Sequence 15, Appl
699	63.5	5.3	397	4	US-09-252-991A-26429	Sequence 26429, A	772	62.5	5.2	161	3	US-09-107-532A-7197	Sequence 7197, Ap
700	63.5	5.3	406	4	US-09-326-033A-23	Sequence 23, Appl	773	62.5	5.2	183	4	US-09-270-767-40648	Sequence 40648, A
701	63.5	5.3	416	4	US-09-328-352-4300	Sequence 4300, Ap	774	62.5	5.2	191	4	US-09-270-767-55864	Sequence 55864, A
702	63.5	5.3	428	4	US-09-799-978-36	Sequence 36, Appl	775	62.5	5.2	191	4	US-09-486-147-40	Sequence 40, Appl
703	63.5	5.3	446	2	US-08-672-814D-11	Sequence 11, Appl	776	62.5	5.2	200	4	US-09-270-767-5126	Sequence 5126, A
704	63.5	5.3	446	3	US-09-333-696-11	Sequence 19, Appl	777	62.5	5.2	200	4	US-09-270-767-36009	Sequence 36009, A
705	63.5	5.3	446	3	US-09-282-218A-19	Sequence 19, Appl	778	62.5	5.2	214	4	US-09-710-279-774	Sequence 774, App
706	63.5	5.3	458	4	US-09-252-991A-20655	Sequence 20655, A	779	62.5	5.2	221	4	US-09-248-796A-15088	Sequence 15088, A
707	63.5	5.3	474	4	US-09-489-039A-10432	Sequence 10432, A	780	62.5	5.2	252	4	US-09-270-767-45203	Sequence 45203, A
708	63.5	5.3	483	1	US-08-194-338-7	Sequence 7, Appli	781	62.5	5.2	261	4	US-09-328-352-6619	Sequence 6619, Ap
709	63.5	5.3	518	4	US-08-543-681A-4949	Sequence 4949, Ap	782	62.5	5.2	304	4	US-09-107-532A-4681	Sequence 4681, Ap
710	63.5	5.3	518	2	US-08-637-759B-89	Sequence 89, Appl	783	62.5	5.2	304	4	US-09-252-991A-22398	Sequence 22398, A
711	63.5	5.3	759	3	US-08-871-355A-89	Sequence 89, Appl	784	62.5	5.2	327	2	US-08-926-724-1	Sequence 1, Appli
712	63.5	5.3	759	3	US-09-201-945-89	Sequence 89, Appl	785	62.5	5.2	341	4	US-09-134-000C-5123	Sequence 5123, Ap
713	63.5	5.3	866	3	US-08-651-999A-1	Sequence 1, Appli	786	62.5	5.2	341	4	US-09-743-871B-1	Sequence 1, Appli
714	63.5	5.3	866	3	US-09-385-752-1	Sequence 2, Appli	787	62.5	5.2	343	4	US-09-743-871B-1	Sequence 1, Appli
715	63.5	5.3	2080	4	US-09-382-552-2	Sequence 45186, A	788	62.5	5.2	343	4	US-09-543-681A-4410	Sequence 4410, Ap
716	63	5.3	147	4	US-09-270-767-45186	Sequence 20, Appl	789	62.5	5.2	345	3	US-09-162-524-3	Sequence 3, Appli
717	63	5.3	177	4	US-09-492-308A-20	Sequence 5495, Ap	790	62.5	5.2	349	4	US-09-762-661A-2	Sequence 2, Appli
718	63	5.3	180	4	US-09-107-532A-5495	Sequence 43, App	791	62.5	5.2	383	5	US-09-330-235-8	Sequence 2, Appli
719	63	5.3	197	4	US-09-198-452A-403	Sequence 403, App	792	62.5	5.2	383	5	PCT-US94-01321-2	Sequence 7223, Ap
720	63	5.3	218	4	US-09-134-000C-4489	Sequence 4489, Ap	793	62.5	5.2	432	4	US-09-489-039A-7223	Sequence 434, App
721	63	5.3	233	3	US-09-134-001C-4013	Sequence 4013, Ap	794	62.5	5.2	432	4	US-09-198-452A-434	Sequence 434, App
722	63	5.3	240	3	US-09-252-991A-29766	Sequence 29766, A	795	62.5	5.2	434	4	US-09-489-039A-13336	Sequence 13336, A
723	63	5.3	259	3	US-09-261-599B-3	Sequence 3, Appli	796	62.5	5.2	439	4	US-09-248-796A-16114	Sequence 16114, A
724	63	5.3	259	3	US-09-456-455A-3	Sequence 3, Appli	797	62.5	5.2	441	4	US-08-121-446-4	Sequence 4, Appli
725	63	5.3	264	4	US-09-270-767-41787	Sequence 41787, A	798	62.5	5.2	442	3	US-09-520-210-10	Sequence 10, Appl
726	63	5.3	295	4	US-09-583-110-4171	Sequence 4171, Ap	799	62.5	5.2	442	3	US-09-161-994A-3	Sequence 3, Appli
727	63	5.3	299	4	US-09-107-532A-5499	Sequence 5499, Ap	800	62.5	5.2	443	3	US-08-117-361C-1	Sequence 1, Appli
728	63	5.3	353	3	US-09-134-001C-3246	Sequence 3246, Ap	801	62.5	5.2	452	1	US-09-710-279-1834	Sequence 1834, Ap
729	63	5.3	359	3	US-08-688-988-32	Sequence 32, Appl	802	62.5	5.2	452	4	US-09-489-039A-10468	Sequence 10468, A
730	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appli	803	62.5	5.2	453	4	US-09-769-863-14	Sequence 9027, Ap
731	63	5.3	361	1	US-08-685-945B-4	Sequence 2, Appli	804	62.5	5.2	453	4	US-09-489-039A-3973	Sequence 3973, Ap
732	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appli	805	62.5	5.2	453	4	US-09-134-001C-3973	Sequence 13646, A
733	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appli	806	62.5	5.2	463	3	US-09-489-039A-13045	Sequence 13045, A
734	63	5.3	370	3	US-09-172-353-3	Sequence 3, Appli	807	62.5	5.2	476	4	US-09-158-767-19	Sequence 19, Appl
735	63	5.3	370	3	US-09-799-955-2	Sequence 3, Appli	808	62.5	5.2	541	3	US-09-158-767-20	Sequence 20, Appl
736	63	5.3	370	4	US-09-799-955-3	Sequence 3, Appli	809	62.5	5.2	541	3	US-09-713-794-19	Sequence 19, Appl
737	63	5.3	370	4	US-09-710-279-2426	Sequence 2426, Ap	810	62.5	5.2	541	4	US-09-713-794-20	Sequence 20, Appl
738	63	5.3	383	4	US-09-134-001C-3437	Sequence 13, Appl	811	62.5	5.2	541	4	US-08-713-794-20	Sequence 6, Appli
739	63	5.3	384	3	US-08-482-746-13	Sequence 13, Appl	812	62.5	5.2	541	4	US-08-424-788-6	Sequence 2, Appli
740	63	5.3	415	4	US-09-580-734-13	Sequence 13, Appl	813	62.5	5.2	557	1	US-08-424-788-5	Sequence 5, Appli
741	63	5.3	415	4	US-08-374-009-13	Sequence 13, Appl	814	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appli
742	63	5.3	415	4	US-09-191-724-13	Sequence 22, Appl	815	62.5	5.2	578	1	US-08-683-743-2	Sequence 2, Appli
743	63	5.3	415	4	US-09-799-978-22	Sequence 12, Appl	816	62.5	5.2	578	2	US-08-477-166-2	Sequence 2, Appli
744	63	5.3	422	3	US-09-625-188-12	Sequence 12, Appl	817	62.5	5.2	578	2	US-08-477-166-2	Sequence 2, Appli
745	63	5.3	431	1	US-08-381-433A-2	Sequence 2, Appli	818	62.5	5.2	578	4	US-09-439-672-2	Sequence 2, Appli
746	63	5.3	431	1	US-09-489-039A-10091	Sequence 10091, A	819	62.5	5.2	578	5	PCT-US93-11638-2	Sequence 7890, Ap
747	63	5.3	441	4	US-08-194-338-5	Sequence 5, Appli	820	62.5	5.2	605	4	US-09-328-352-7890	Sequence 5288, Ap
748	63	5.3	450	1	US-08-444-734A-8	Sequence 8, Appli	821	62.5	5.2	605	4	US-09-107-532A-5288	Sequence 19, Appl
749	63	5.3	451	3	US-09-134-001C-4420	Sequence 4420, Ap	822	62.5	5.2	628	4	US-09-342-647-18	Sequence 6690, Ap
750	63	5.3	489	2	US-09-062-890-36	Sequence 34, Appl	823	62.5	5.2	669	3	US-09-134-000C-6690	Sequence 40617, A
751	63	5.3	489	2	US-08-890-980-2	Sequence 36, Appl	824	62.5	5.2	785	4	US-09-270-767-40617	Sequence 55833, A
752	63	5.3	509	3	US-08-890-979-2	Sequence 2, Appli	825	62.5	5.2	796	4	US-09-270-767-55833	Sequence 11704, A
753	63	5.3	509	3	US-09-032-894-2	Sequence 2, Appli	826	62.5	5.2	796	4	US-09-489-039A-11704	Sequence 23462, A
754	63	5.3	509	3	US-09-031-626-2	Sequence 2, Appli	827	62.5	5.2	1768	4	US-09-248-796A-23462	Sequence 5183, A
755	63	5.3	509	3	US-09-054-272-59	Sequence 59, Appl	828	62	5.2	112	4	US-09-270-767-59183	Sequence 10, Appl
756	63	5.3	509	4			829	62	5.2	129	4	US-09-673-898-10	
757	63	5.3	509	4			830	62	5.2				

831	62	5.2	250	4	US-09-270-767-43784	Sequence 43784, A	904	61.5	5.1	271	3	US-09-077-675A-12	Sequence 12, Appl
832	62	5.2	254	4	US-09-248-796A-22532	Sequence 22532, A	905	61.5	5.1	271	4	US-09-077-674-12	Sequence 12, Appl
833	62	5.2	272	4	US-09-903-456-76	Sequence 76, Appl	906	61.5	5.1	288	4	US-09-134-000C-5520	Sequence 5520, Ap
834	62	5.2	272	4	US-09-903-456-80	Sequence 80, Appl	907	61.5	5.1	289	4	US-09-489-039A-12390	Sequence 12390, A
835	62	5.2	272	4	US-09-903-456-81	Sequence 81, Appl	908	61.5	5.1	297	4	US-09-328-352-5769	Sequence 5769, Ap
836	62	5.2	283	4	US-09-903-456-88	Sequence 88, Appl	909	61.5	5.1	302	3	US-09-077-675A-2	Sequence 2, Appli
837	62	5.2	288	4	US-09-903-456-84	Sequence 84, Appl	910	61.5	5.1	302	3	US-09-077-675A-7	Sequence 7, Appli
838	62	5.2	290	3	US-09-134-001C-4893	Sequence 4893, Ap	911	61.5	5.1	302	4	US-09-077-674-2	Sequence 2, Appli
839	62	5.2	292	4	US-09-903-456-82	Sequence 82, Appl	912	61.5	5.1	302	4	US-09-077-674-7	Sequence 7, Appli
840	62	5.2	295	4	US-09-903-456-86	Sequence 86, Appl	913	61.5	5.1	332	4	US-09-543-681A-6853	Sequence 6853, Ap
841	62	5.2	305	4	US-09-270-767-44944	Sequence 44944, A	914	61.5	5.1	349	4	US-09-270-767-38347	Sequence 38347, A
842	62	5.2	317	4	US-09-489-039A-9602	Sequence 9602, A	915	61.5	5.1	349	4	US-09-270-767-53564	Sequence 53564, A
843	62	5.2	323	1	US-07-667-276A-7	Sequence 7, Appli	916	61.5	5.1	353	3	US-09-077-675A-3	Sequence 3, Appli
844	62	5.2	326	4	US-09-543-681A-7161	Sequence 7161, Ap	917	61.5	5.1	353	3	US-09-077-674-3	Sequence 3, Appli
845	62	5.2	331	2	US-08-560-98A-46	Sequence 46, Appl	918	61.5	5.1	361	3	US-09-077-675A-8	Sequence 8, Appli
846	62	5.2	355	1	US-07-759-568-1	Sequence 1, Appli	919	61.5	5.1	361	4	US-09-077-674-8	Sequence 8, Appli
847	62	5.2	355	1	US-08-450-393A-8	Sequence 8, Appli	920	61.5	5.1	366	3	US-09-077-675A-13	Sequence 13, Appl
848	62	5.2	355	2	US-08-390-000A-5	Sequence 5, Appli	921	61.5	5.1	366	4	US-09-077-674-13	Sequence 13, Appl
849	62	5.2	355	3	US-08-446-669-8	Sequence 8, Appli	922	61.5	5.1	366	4	US-09-170-496D-88	Sequence 88, Appl
850	62	5.2	355	3	US-09-045-583-53	Sequence 53, Appl	923	61.5	5.1	366	4	US-09-743-742B-7	Sequence 7, Appli
851	62	5.2	355	4	US-09-534-185-53	Sequence 53, Appl	924	61.5	5.1	366	4	US-09-762-661A-7	Sequence 5, Appli
852	62	5.2	355	4	US-09-525-573-8	Sequence 8, Appli	925	61.5	5.1	366	4	US-09-762-661A-5	Sequence 7, Appli
853	62	5.2	355	5	PCT-US95-00476-8	Sequence 8, Appli	926	61.5	5.1	366	4	US-09-364-425B-45	Sequence 45, Appl
854	62	5.2	360	1	US-08-202-056-7	Sequence 7, Appli	927	61.5	5.1	366	4	US-09-743-475-4	Sequence 4, Appli
855	62	5.2	360	1	US-08-597-236-11	Sequence 11, Appl	928	61.5	5.1	366	4	US-09-743-475-6	Sequence 6, Appli
856	62	5.2	360	1	US-08-746-582A-11	Sequence 11, Appl	929	61.5	5.1	376	2	US-08-465-976A-3	Sequence 3, Appli
857	62	5.2	360	4	US-09-409-778-4	Sequence 4, Appli	930	61.5	5.1	376	2	US-08-982-412-3	Sequence 3, Appli
858	62	5.2	384	4	US-09-710-279-184	Sequence 184, App	931	61.5	5.1	379	3	US-09-740-035-4	Sequence 4, Appli
859	62	5.2	384	4	US-09-491-577-16	Sequence 16, Appl	932	61.5	5.1	391	1	US-07-921-178A-2	Sequence 2, Appli
860	62	5.2	393	4	US-09-252-991A-25633	Sequence 25633, A	933	61.5	5.1	391	1	US-08-103-445-5	Sequence 5, Appli
861	62	5.2	405	4	US-09-489-039A-7574	Sequence 7574, Ap	934	61.5	5.1	391	1	US-08-461-690B-5	Sequence 5, Appli
862	62	5.2	409	4	US-09-583-110-3749	Sequence 3749, Ap	935	61.5	5.1	391	2	US-08-501-003A-16	Sequence 16, Appl
863	62	5.2	412	3	US-09-134-001C-3949	Sequence 3949, Ap	936	61.5	5.1	391	4	US-09-275-252A-13	Sequence 13, Appl
864	62	5.2	414	4	US-09-198-452A-414	Sequence 414, App	937	61.5	5.1	392	4	US-09-489-039A-8713	Sequence 8713, Ap
865	62	5.2	415	4	US-09-799-978-28	Sequence 28, Appl	938	61.5	5.1	397	4	US-09-491-577-32	Sequence 32, Appl
866	62	5.2	417	4	US-09-710-279-950	Sequence 950, App	939	61.5	5.1	411	2	US-08-741-134-6	Sequence 6, Appli
867	62	5.2	447	4	US-09-388-089B-2	Sequence 2, Appli	940	61.5	5.1	415	1	US-08-110-286A-6	Sequence 6, Appli
868	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl	941	61.5	5.1	415	3	US-08-981-189B-10	Sequence 10, Appl
869	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl	942	61.5	5.1	415	3	US-08-482-746-6	Sequence 6, Appli
870	62	5.2	475	4	US-09-388-089B-12	Sequence 12, Appl	943	61.5	5.1	415	4	US-09-580-734-6	Sequence 6, Appli
871	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl	944	61.5	5.1	415	4	US-08-374-009-6	Sequence 6, Appli
872	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl	945	61.5	5.1	415	4	US-09-191-724-6	Sequence 6, Appli
873	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl	946	61.5	5.1	415	4	US-09-799-978-16	Sequence 16, Appl
874	62	5.2	489	2	US-09-020-991-14	Sequence 14, Appl	947	61.5	5.1	417	4	US-09-252-991A-26638	Sequence 26638, A
875	62	5.2	489	2	US-09-020-991-22	Sequence 22, Appl	948	61.5	5.1	418	4	US-09-543-681A-7634	Sequence 7634, Ap
876	62	5.2	489	2	US-09-020-991-24	Sequence 24, Appl	949	61.5	5.1	427	4	US-09-922-501-2	Sequence 2, Appli
877	62	5.2	489	2	US-09-062-890-14	Sequence 14, Appl	950	61.5	5.1	458	4	US-09-252-991A-28897	Sequence 28897, A
878	62	5.2	489	2	US-09-062-890-22	Sequence 22, Appl	951	61.5	5.1	469	4	US-08-956-171B-5245	Sequence 5245, Ap
879	62	5.2	489	2	US-09-062-890-24	Sequence 24, Appl	952	61.5	5.1	469	4	US-08-781-986A-5245	Sequence 5245, Ap
880	62	5.2	498	4	US-09-388-089B-11	Sequence 11, Appl	953	61.5	5.1	479	2	US-08-899-514-2	Sequence 2, Appli
881	62	5.2	499	4	US-09-673-898-6	Sequence 6, Appli	954	61.5	5.1	497	1	US-08-295-670-6	Sequence 6, Appli
882	62	5.2	557	3	US-09-560-639-7	Sequence 7, Appli	955	61.5	5.1	497	1	US-08-633-485-6	Sequence 6, Appli
883	62	5.2	567	3	US-09-173-151A-24	Sequence 24, Appl	956	61.5	5.1	510	3	US-09-134-001C-3368	Sequence 3368, Ap
884	62	5.2	567	3	US-09-032-337-39	Sequence 39, Appl	957	61.5	5.1	524	2	US-08-853-659A-35	Sequence 35, Appl
885	62	5.2	582	3	US-08-194-560-2	Sequence 2, Appli	958	61.5	5.1	524	1	US-08-298-426-4	Sequence 4, Appli
886	62	5.2	602	3	US-09-134-001C-4416	Sequence 4416, Ap	959	61.5	5.1	615	4	US-09-602-787A-534	Sequence 534, App
887	62	5.2	638	3	US-09-376-781-6	Sequence 6, Appli	960	61.5	5.1	615	4	US-09-602-787A-536	Sequence 536, App
888	62	5.2	706	4	US-09-538-092-957	Sequence 957, App	961	61.5	5.1	659	4	US-09-583-110-3110	Sequence 3110, Ap
889	62	5.2	775	3	US-09-305-640-2	Sequence 2, Appli	962	61.5	5.1	674	4	US-09-538-092-1125	Sequence 1125, Ap
890	62	5.2	775	4	US-10-140-002-120	Sequence 120, App	963	61.5	5.1	685	4	US-09-720-317A-31	Sequence 31, Appl
891	62	5.2	800	4	US-09-248-796A-20101	Sequence 20101, A	964	61.5	5.1	685	4	US-09-248-796A-18612	Sequence 18612, A
892	62	5.2	1186	1	US-08-602-737-6	Sequence 6, Appli	965	61.5	5.1	817	1	US-08-381-931B-2	Sequence 2, Appli
893	62	5.2	1186	3	US-09-001-982-6	Sequence 6, Appli	966	61.5	5.1	895	4	US-09-489-039A-13127	Sequence 13127, A
894	62	5.2	1186	4	US-09-668-650-6	Sequence 6, Appli	967	61.5	5.1	965	4	US-09-437-277-3	Sequence 3, Appli
895	62	5.2	1267	4	US-09-543-681A-6130	Sequence 6130, Ap	968	61.5	5.1	1025	4	US-09-543-681A-7112	Sequence 7112, Ap
896	62	5.2	1985	4	US-09-495-714C-6	Sequence 6, Appli	969	61.5	5.1	1025	4	US-09-091-219-25	Sequence 25, Appl
897	61.5	5.1	163	3	US-08-600-430-4	Sequence 4, Appli	970	61.5	5.1	2232	3	US-09-860-541-25	Sequence 25, Appl
898	61.5	5.1	170	4	US-09-710-279-1164	Sequence 1164, Ap	971	61.5	5.1	2232	3	US-09-091-219-2	Sequence 2, Appli
899	61.5	5.1	186	3	US-09-134-001C-4095	Sequence 4095, Ap	972	61.5	5.1	2247	3	US-09-660-541-2	Sequence 12, Appl
900	61.5	5.1	235	3	US-08-812-586-16	Sequence 16, Appl	973	61.5	5.1	2247	3	US-08-952-127-12	Sequence 12, Appl
901	61.5	5.1	235	4	US-09-535-832A-17	Sequence 17, Appl	974	61	5.1	95	4	US-09-248-796A-21665	Sequence 21665, A
902	61.5	5.1	260	4	US-09-540-236-3812	Sequence 3812, Ap	975	61	5.1	122	4	US-09-710-279-102	Sequence 102, App
903	61.5	5.1	269	4	US-09-489-039A-9180	Sequence 9180, Ap	976	61	5.1	175	2	US-08-408-095-11	Sequence 11, Appl

977	61	5.1	188	4	US-09-198-452A-1206	Sequence 1206, Ap	1050	60.5	5.1	199	3	US-09-019-793A-33	Sequence 33, Appl
978	61	5.1	189	3	US-09-080-643-4	Sequence 4, Appl	1051	60.5	5.1	200	2	US-08-799-464A-9	Sequence 9, Appl
979	61	5.1	200	4	US-09-710-279-394	Sequence 394, App	1052	60.5	5.1	200	4	US-09-601-326-33	Sequence 33, Appl
980	61	5.1	200	4	US-09-710-279-1242	Sequence 1242, Ap	1053	60.5	5.1	200	5	PCT-US95-09927-9	Sequence 9, Appl
981	61	5.1	206	3	US-09-134-001C-3929	Sequence 3929, Ap	1054	60.5	5.1	207	4	US-08-811-519-18	Sequence 18, Appl
982	61	5.1	206	3	US-09-134-001C-3929	Sequence 3929, Ap	1055	60.5	5.1	222	4	US-09-270-767-42973	Sequence 42973, A
983	61	5.1	207	3	US-08-559-397A-13	Sequence 11, Appl	1056	60.5	5.1	224	2	US-09-270-767-42973	Sequence 6, Appl
984	61	5.1	209	3	US-08-559-397A-11	Sequence 30213, A	1057	60.5	5.1	240	3	US-08-114-555A-6	Sequence 12, Appl
985	61	5.1	225	4	US-09-252-991A-30213	Sequence 30213, Ap	1058	60.5	5.1	240	3	US-08-559-397A-12	Sequence 2276, A
986	61	5.1	230	3	US-09-134-001C-3744	Sequence 3744, Ap	1059	60.5	5.1	269	3	US-08-796A-22276	Sequence 6, Appl
987	61	5.1	239	4	US-09-710-279-978	Sequence 978, App	1060	60.5	5.1	280	3	US-08-652-877-6	Sequence 6, Appl
988	61	5.1	241	4	US-09-489-039A-8397	Sequence 8397, Ap	1061	60.5	5.1	280	3	US-08-476-515A-6	Sequence 78, Appl
989	61	5.1	256	1	US-08-236-918A-6	Sequence 6, Appl	1062	60.5	5.1	283	5	US-08-118-270-78	Sequence 37, Appl
990	61	5.1	256	3	US-09-012-269A-6	Sequence 6, Appl	1063	60.5	5.1	285	4	PCT-US93-08528-78	Sequence 78, Appl
991	61	5.1	256	3	US-08-623-545A-3	Sequence 2, Appl	1064	60.5	5.1	296	4	US-10-162-012-37	Sequence 37, Appl
992	61	5.1	256	5	PCT-US96-03965-2	Sequence 3, Appl	1065	60.5	5.1	300	4	US-09-540-236-2856	Sequence 2856, Ap
993	61	5.1	261	3	US-09-134-001C-3485	Sequence 3485, Ap	1066	60.5	5.1	301	4	US-09-393-634-17	Sequence 17, Appl
994	61	5.1	261	3	US-09-107-532A-6716	Sequence 6716, Ap	1067	60.5	5.1	342	2	US-08-742-011-2	Sequence 166, App
995	61	5.1	272	4	US-09-903-456-78	Sequence 78, Appl	1068	60.5	5.1	342	2	US-08-742-011-2	Sequence 2, Appl
996	61	5.1	277	4	US-09-583-110-3171	Sequence 3171, Ap	1069	60.5	5.1	342	3	US-09-275-384B-5	Sequence 2, Appl
997	61	5.1	285	4	US-09-543-681A-7666	Sequence 7666, Ap	1070	60.5	5.1	342	3	US-09-116-498-2	Sequence 9, Appl
998	61	5.1	296	4	US-09-540-236-2583	Sequence 2583, Ap	1071	60.5	5.1	342	3	US-09-449-437A-2	Sequence 2, Appl
999	61	5.1	302	4	US-08-311-731A-173	Sequence 173, App	1072	60.5	5.1	342	3	US-09-517-605-9	Sequence 9, Appl
1000	61	5.1	338	4	US-09-107-532A-6222	Sequence 6222, Ap	1073	60.5	5.1	342	4	US-09-852-156-2	Sequence 2, Appl
1001	61	5.1	345	4	US-09-107-532A-5817	Sequence 5817, Ap	1074	60.5	5.1	352	4	US-09-710-279-932	Sequence 932, App
1002	61	5.1	355	4	US-09-489-039A-7417	Sequence 7417, Ap	1075	60.5	5.1	357	4	US-09-489-039A-9155	Sequence 9155, Ap
1003	61	5.1	355	4	US-08-833-752-8	Sequence 8, Appl	1076	60.5	5.1	357	4	US-09-107-532A-5132	Sequence 5, Appl
1004	61	5.1	355	4	US-09-938-719-8	Sequence 8, Appl	1077	60.5	5.1	358	4	US-08-743-130A-2	Sequence 2, Appl
1005	61	5.1	358	4	US-09-248-796A-19081	Sequence 19081, A	1078	60.5	5.1	388	4	US-09-107-532A-4918	Sequence 39, Appl
1006	61	5.1	363	3	US-08-688-988A-30	Sequence 30, Appl	1079	60.5	5.1	409	2	US-08-743-130A-2	Sequence 39, Appl
1007	61	5.1	408	4	US-09-328-352-5768	Sequence 5768, Ap	1080	60.5	5.1	417	4	US-09-248-796A-16410	Sequence 4, Appl
1008	61	5.1	440	4	US-09-489-039A-12132	Sequence 12132, A	1081	60.5	5.1	424	3	US-09-161-994A-4	Sequence 9587, Ap
1009	61	5.1	445	4	US-09-799-978-34	Sequence 34, Appl	1082	60.5	5.1	446	4	US-09-489-039A-9587	Sequence 5044, Ap
1010	61	5.1	481	4	US-09-248-796A-18683	Sequence 18683, A	1083	60.5	5.1	451	4	US-09-328-352-5044	Sequence 1459, A
1011	61	5.1	488	4	US-09-248-796A-15101	Sequence 15101, A	1084	60.5	5.1	473	4	US-09-489-039A-14199	Sequence 1459, A
1012	61	5.1	489	4	US-09-710-279-2632	Sequence 2632, Ap	1085	60.5	5.1	475	4	US-09-270-767-43475	Sequence 43475, A
1013	61	5.1	500	4	US-09-134-000C-4886	Sequence 4886, Ap	1086	60.5	5.1	487	3	US-09-724-224-4	Sequence 8, Appl
1014	61	5.1	503	3	US-09-556-916-36	Sequence 26, Appl	1087	60.5	5.1	487	3	US-10-093-317-8	Sequence 2, Appl
1015	61	5.1	672	4	US-09-556-916-36	Sequence 26, Appl	1088	60.5	5.1	489	4	US-09-986-536-2	Sequence 19910, A
1016	61	5.1	672	4	US-09-556-916-36	Sequence 26, Appl	1089	60.5	5.1	490	4	US-09-248-796A-19910	Sequence 5082, Ap
1017	61	5.1	724	4	US-09-252-991A-30228	Sequence 30228, A	1090	60.5	5.1	490	4	US-09-107-532A-5082	Sequence 294, Ap
1018	61	5.1	737	4	US-09-248-796A-14319	Sequence 14319, A	1091	60.5	5.1	498	4	US-09-583-110-2949	Sequence 1558, Ap
1019	61	5.1	746	4	US-09-248-796A-17109	Sequence 17109, A	1092	60.5	5.1	498	4	US-09-710-279-1558	Sequence 24, Appl
1020	61	5.1	806	4	US-09-833-466-13	Sequence 13, Appl	1093	60.5	5.1	499	4	US-09-068-195-24	Sequence 4, Appl
1021	61	5.1	848	4	US-09-583-110-2738	Sequence 2738, Ap	1094	60.5	5.1	503	3	US-09-724-224-4	Sequence 4, Appl
1022	61	5.1	880	4	US-09-538-092-577	Sequence 577, App	1095	60.5	5.1	512	3	US-10-093-317-4	Sequence 20852, A
1023	61	5.1	915	4	US-09-107-532A-3714	Sequence 3714, Ap	1096	60.5	5.1	512	3	US-09-248-796A-20852	Sequence 7452, Ap
1024	61	5.1	1299	4	US-09-252-991A-31121	Sequence 31121, A	1097	60.5	5.1	519	4	US-09-489-039A-7452	Sequence 5507, Ap
1025	61	5.1	1503	4	US-09-600-087-2	Sequence 2, Appl	1098	60.5	5.1	533	4	US-09-107-532A-5507	Sequence 4091, Ap
1026	61	5.1	2864	4	US-08-469-260A-394	Sequence 394, App	1099	60.5	5.1	536	4	US-09-134-001C-4091	Sequence 5109, Ap
1027	61	5.1	2864	4	US-08-488-446-394	Sequence 394, App	1100	60.5	5.1	537	3	US-09-343-681A-5774	Sequence 2943, Ap
1028	61	5.1	2864	4	US-08-467-344A-394	Sequence 394, App	1101	60.5	5.1	554	3	US-09-540-236-2943	Sequence 35, Appl
1029	61	5.1	2864	4	US-08-424-550B-394	Sequence 20, Appl	1102	60.5	5.1	558	4	US-09-595-684B-35	Sequence 4499, Ap
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1031	61	5.1	3011	3	US-09-014-416-1	Sequence 20, Appl	1104	60.5	5.1	682	4	US-09-248-796A-20210	Sequence 6007, Ap
1032	61	5.1	3011	3	US-09-034-756-20	Sequence 1, Appl	1105	60.5	5.1	694	4	US-09-612-204B-24	Sequence 24, Appl
1033	61	5.1	3011	4	US-10-104-966-1	Sequence 9, Appl	1106	60.5	5.1	736	4	US-09-248-796A-16640	Sequence 16640, A
1034	61	5.1	3012	3	US-09-952-572-9	Sequence 2, Appl	1107	60.5	5.1	865	4	US-09-270-767-46728	Sequence 46728, A
1035	61	5.1	3012	3	US-08-811-566-2	Sequence 2, Appl	1108	60.5	5.1	1064	4	US-09-270-767-46728	Sequence 2, Appl
1036	61	5.1	3012	3	US-09-034-756-2	Sequence 2, Appl	1109	60.5	5.1	1323	4	US-08-913-832A-2	Sequence 2, Appl
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1039	60.5	5.1	116	4	US-09-270-767-36280	Sequence 36280, A	1112	60.5	5.1	1912	4	US-09-538-092-979	Sequence 31761, A
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1041	60.5	5.1	137	4	US-09-270-767-32124	Sequence 32124, A	1114	60.5	5.1	136	4	US-09-270-767-46978	Sequence 4993, Ap
1042	60.5	5.1	157	4	US-09-270-767-47341	Sequence 47341, A	1115	60	5.0	162	4	US-09-134-000C-4993	Sequence 23, Appl
1043	60.5	5.1	157	4	US-09-270-767-47341	Sequence 47341, A	1116	60	5.0	177	4	US-09-492-308A-23	Sequence 3341, A
1044	60.5	5.1	157	4	US-09-270-767-58298	Sequence 58298, A	1117	60	5.0	177	4	US-09-080-643-2	Sequence 47558, Ap
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1046	60.5	5.1	194	4	US-09-270-767-34926	Sequence 34926, A	1119	60	5.0	189	3	US-09-270-767-32341	Sequence 3197, Ap
1047	60.5	5.1	195	4	US-09-270-767-50143	Sequence 50143, A	1120	60	5.0	189	3	US-09-270-767-32341	Sequence 3197, Ap
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1049	60.5	5.1	199	3	US-09-270-767-58832	Sequence 58832, A	1122	60	5.0	191	4	US-09-583-110-3197	Sequence 3197, Ap

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1124	60	5.0	206	3	US-08-513-974B-27	Sequence 27, Appl	1197	60	5.0	1137	4	US-09-352-391A-24829	Sequence 24829, A
1125	60	5.0	206	3	US-08-776-971-22	Sequence 27, Appl	1198	60	5.0	1156	4	US-09-198-452A-171	Sequence 171, App
1126	60	5.0	206	4	US-09-461-436B-27	Sequence 27, Appl	1199	60	5.0	1296	2	US-08-857-636-60	Sequence 60, Appl
1127	60	5.0	206	4	US-09-576-290-22	Sequence 22, Appl	1200	60	5.0	1447	2	US-08-540-406-19	Sequence 19, Appl
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1130	60	5.0	223	3	US-08-513-974B-364	Sequence 364, App	1203	60	5.0	1447	3	US-09-268-140-5	Sequence 5, Appli
1131	60	5.0	223	3	US-08-513-974B-368	Sequence 368, App	1204	60	5.0	1447	4	US-08-918-658-19	Sequence 19, Appl
1132	60	5.0	223	3	US-08-776-971-100	Sequence 100, App	1205	60	5.0	1447	4	US-09-724-631-19	Sequence 19, Appl
1133	60	5.0	223	3	US-08-776-971-102	Sequence 102, App	1206	60	5.0	1447	4	US-08-954-701A-19	Sequence 19, Appl
1134	60	5.0	223	3	US-08-776-971-108	Sequence 108, App	1207	60	5.0	1447	5	PCT-US95-13233-19	Sequence 19, Appl
1135	60	5.0	223	4	US-09-576-290-100	Sequence 100, App	1208	60	5.0	2235	4	US-09-032-438C-6	Sequence 6, Appli
1136	60	5.0	223	4	US-09-576-290-102	Sequence 102, App	1209	60	5.0	2273	4	US-09-032-438C-3	Sequence 3, Appli
1137	60	5.0	223	4	US-09-576-290-108	Sequence 108, App	1210	60	5.0	3011	1	US-08-453-552-2	Sequence 2, Appli
1138	60	5.0	242	3	US-08-908-332-2	Sequence 2, Appli	1211	60	5.0	3011	2	US-08-710-637-2	Sequence 2, Appli
1139	60	5.0	257	4	US-09-543-681A-6362	Sequence 6362, Ap	1212	60	5.0	3011	5	PCT-US93-00907-2	Sequence 2, Appli
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1141	60	5.0	282	4	US-09-270-767-35685	Sequence 35685, A	1214	59.5	5.0	159	4	US-09-248-796A-27840	Sequence 27840, A
1142	60	5.0	282	4	US-09-270-767-50902	Sequence 50902, A	1215	59.5	5.0	161	4	US-09-270-767-36990	Sequence 36990, A
1143	60	5.0	284	4	US-09-252-991A-26771	Sequence 26771, A	1216	59.5	5.0	161	4	US-09-270-767-52207	Sequence 52207, A
1144	60	5.0	285	3	US-09-095-758-10	Sequence 10, Appl	1217	59.5	5.0	195	2	US-08-467-822-44	Sequence 44, Appl
1145	60	5.0	295	3	US-09-422-968-10	Sequence 10, Appl	1218	59.5	5.0	195	2	US-08-211-312-3	Sequence 3, Appli
1146	60	5.0	295	4	US-09-708-015A-10	Sequence 10, Appl	1219	59.5	5.0	195	3	US-08-472-285-3	Sequence 3, Appli
1147	60	5.0	313	4	US-09-270-767-58683	Sequence 58683, A	1220	59.5	5.0	195	3	US-09-107-383-10	Sequence 10, Appl
1148	60	5.0	317	3	US-08-605-284B-17	Sequence 17, Appl	1221	59.5	5.0	195	3	US-08-432-697-44	Sequence 44, Appl
1149	60	5.0	324	4	US-09-543-681A-6241	Sequence 6241, Ap	1222	59.5	5.0	195	3	US-08-466-248-44	Sequence 44, Appl
1150	60	5.0	326	4	US-09-540-236-3340	Sequence 3340, Ap	1223	59.5	5.0	195	3	US-08-472-929-3	Sequence 3, Appli
1151	60	5.0	328	4	US-09-543-681A-5252	Sequence 5252, Ap	1224	59.5	5.0	195	4	US-09-643-914-10	Sequence 10, Appl
1152	60	5.0	330	4	US-09-543-681A-7116	Sequence 7116, Ap	1225	59.5	5.0	195	4	US-09-742-361A-10	Sequence 10, Appl
1153	60	5.0	333	4	US-09-170-496D-8	Sequence 8, Appli	1226	59.5	5.0	199	3	US-08-478-316-37	Sequence 37, Appl
1154	60	5.0	333	4	US-09-170-496D-168	Sequence 168, App	1227	59.5	5.0	199	3	US-09-019-793A-37	Sequence 37, Appl
1155	60	5.0	347	4	US-09-107-532A-6019	Sequence 6019, Ap	1228	59.5	5.0	199	4	US-09-601-326-37	Sequence 37, Appl
1156	60	5.0	359	4	US-09-107-532A-6455	Sequence 6455, Ap	1229	59.5	5.0	209	4	US-09-248-796A-16080	Sequence 16080, A
1157	60	5.0	360	4	US-09-270-767-32827	Sequence 32827, A	1230	59.5	5.0	220	4	US-09-107-532A-6803	Sequence 6803, Ap
1158	60	5.0	360	4	US-09-270-767-32827	Sequence 32827, A	1231	59.5	5.0	232	4	US-09-107-532A-6747	Sequence 6747, Ap
1159	60	5.0	376	4	US-09-107-532A-6448	Sequence 6448, Ap	1232	59.5	5.0	249	4	US-09-328-352-4690	Sequence 4690, Ap
1160	60	5.0	377	3	US-09-316-080-5	Sequence 5, Appli	1233	59.5	5.0	275	4	US-09-371-056-10	Sequence 10, Appl
1161	60	5.0	382	3	US-09-134-001C-4483	Sequence 4483, Ap	1234	59.5	5.0	280	4	US-09-543-681A-6175	Sequence 6175, Ap
1162	60	5.0	387	2	US-08-902-853-6	Sequence 6, Appli	1235	59.5	5.0	281	4	US-09-134-000C-4344	Sequence 4344, Ap
1163	60	5.0	397	2	US-08-990-379-8	Sequence 8, Appli	1236	59.5	5.0	293	4	US-09-107-532A-4206	Sequence 4206, Ap
1164	60	5.0	416	4	US-09-583-110-2732	Sequence 2732, Ap	1237	59.5	5.0	295	4	US-09-543-681A-5660	Sequence 5660, Ap
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1166	60	5.0	419	1	US-08-385-186-2	Sequence 4, Appli	1239	59.5	5.0	327	3	US-08-904-032-3	Sequence 3, Appli
1167	60	5.0	419	1	US-08-385-186-4	Sequence 4, Appli	1240	59.5	5.0	337	4	US-09-540-236-2590	Sequence 2590, Ap
1168	60	5.0	419	4	US-09-270-767-43338	Sequence 43338, A	1241	59.5	5.0	341	1	US-08-423-564-5	Sequence 5, Appli
1169	60	5.0	420	4	US-09-799-978-42	Sequence 42, Appl	1242	59.5	5.0	350	1	US-08-118-270-41	Sequence 41, Appl
1170	60	5.0	421	4	US-09-543-681A-7791	Sequence 7791, Ap	1243	59.5	5.0	350	4	US-09-910-695-8	Sequence 8, Appli
1171	60	5.0	422	4	US-09-540-236-2283	Sequence 2283, Ap	1244	59.5	5.0	350	5	PCT-US93-08528-41	Sequence 41, Appl
1172	60	5.0	448	3	US-09-134-001C-4146	Sequence 4146, Ap	1245	59.5	5.0	369	4	US-09-543-681A-6725	Sequence 6725, Ap
1173	60	5.0	467	3	US-08-867-611-28	Sequence 28, Appl	1246	59.5	5.0	370	3	US-09-134-001C-4166	Sequence 4166, Ap
1174	60	5.0	467	4	US-09-690-359-28	Sequence 28, Appl	1247	59.5	5.0	388	4	US-09-222-938A-37	Sequence 37, Appl
1175	60	5.0	467	5	PCT-US92-06965A-33	Sequence 33, Appl	1248	59.5	5.0	399	4	US-09-583-110-2855	Sequence 2855, Ap
1176	60	5.0	502	1	US-08-484-840-3	Sequence 3, Appli	1249	59.5	5.0	411	2	US-08-933-750C-24	Sequence 24, Appl
1177	60	5.0	502	1	US-08-483-094-3	Sequence 3, Appli	1250	59.5	5.0	431	3	US-09-234-613-24	Sequence 24, Appl
1178	60	5.0	509	4	US-09-134-000C-5949	Sequence 5949, Ap	1251	59.5	5.0	439	2	US-08-853-659A-37	Sequence 37, Appl
1179	60	5.0	521	4	US-09-538-092-1330	Sequence 1330, Ap	1252	59.5	5.0	444	4	US-09-540-236-1993	Sequence 1993, Ap
1180	60	5.0	521	5	PCT-US93-08386-10	Sequence 10, Appl	1253	59.5	5.0	445	4	US-09-710-279-2644	Sequence 2644, Ap
1181	60	5.0	587	4	US-09-538-092-1130	Sequence 1130, Ap	1254	59.5	5.0	447	4	US-09-694-519-9	Sequence 9, Appli
1182	60	5.0	590	3	US-08-893-852A-4	Sequence 4, Appli	1255	59.5	5.0	471	4	US-09-543-681A-4195	Sequence 4195, Ap
1183	60	5.0	590	3	US-08-821-818-2	Sequence 2, Appli	1256	59.5	5.0	533	4	US-09-248-796A-14472	Sequence 14472, A
1184	60	5.0	596	4	US-09-052-753B-2	Sequence 2, Appli	1257	59.5	5.0	606	4	US-09-107-532A-4683	Sequence 4683, Ap
1185	60	5.0	626	1	US-07-938-782A-2	Sequence 2, Appli	1258	59.5	5.0	649	3	US-09-134-001C-3891	Sequence 3891, Ap
1186	60	5.0	626	1	US-08-630-524-2	Sequence 2, Appli	1259	59.5	5.0	662	4	US-09-352-991A-22861	Sequence 22861, A
1187	60	5.0	626	4	US-09-578-441-5	Sequence 5, Appli	1260	59.5	5.0	680	2	US-08-674-351-2	Sequence 2, Appli
1188	60	5.0	626	5	PCT-US93-08131-2	Sequence 2, Appli	1261	59.5	5.0	738	4	US-09-328-352-4315	Sequence 4315, Ap
1189	60	5.0	630	4	US-09-602-787A-548	Sequence 548, App	1262	59.5	5.0	739	1	US-07-803-622B-2	Sequence 2, Appli
1190	60	5.0	633	3	US-09-134-001C-5661	Sequence 5661, Ap	1263	59.5	5.0	753	4	US-09-252-991A-17631	Sequence 17631, A
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1192	60	5.0	724	3	US-09-307-143-6	Sequence 6, Appli	1265	59.5	5.0	852	4	US-09-081-385-153	Sequence 153, App
1193	60	5.0	730	4	US-09-328-352-4442	Sequence 4442, Ap	1266	59.5	5.0	961	4	US-09-328-352-4182	Sequence 4182, Ap
1194	60	5.0	734	4	US-09-585-858-9	Sequence 9, Appli	1267	59.5	5.0	975	4	US-09-540-236-2304	Sequence 2304, Ap
1195	60	5.0	770	4	US-09-252-991A-28510	Sequence 28510, A	1268	59.5	5.0	1040	4	US-09-328-352-7238	Sequence 7238, Ap

1269	59.5	5.0	1248	3	US-08-726-214-16	Sequence 16, Appl	1342	59	4.9	586	4	US-09-107-532A-6918	Sequence 6918, Ap
1270	59.5	5.0	1466	4	US-09-262-537-20	Sequence 20, Appl	1343	59	4.9	591	1	US-08-179-738-10	Sequence 10, Appl
1271	59.5	5.0	1469	4	US-09-262-537-58	Sequence 58, Appl	1344	59	4.9	591	2	US-08-628-145-10	Sequence 10, Appl
1272	59.5	5.0	1471	4	US-08-811-519-1	Sequence 1, Appl	1345	59	4.9	595	1	US-08-171-718-16	Sequence 16, Appl
1273	59.5	5.0	1876	2	US-08-619-554-2	Sequence 2, Appl	1346	59	4.9	595	3	US-08-478-087-16	Sequence 16, Appl
1274	59.5	5.0	2273	3	US-09-426-998-5	Sequence 5, Appl	1347	59	4.9	596	1	US-08-179-738-3	Sequence 3, Appl
1275	59.5	5.0	2386	1	US-08-157-005-2	Sequence 2, Appl	1348	59	4.9	596	2	US-08-628-145-3	Sequence 3, Appl
1276	59.5	5.0	2386	3	US-08-747-863-2	Sequence 2, Appl	1349	59	4.9	600	4	US-09-134-000C-5694	Sequence 5694, Ap
1277	59.5	5.0	3033	1	US-09-565-864-2	Sequence 2, Appl	1350	59	4.9	620	4	US-08-959-004-10	Sequence 10, Appl
1278	59.5	5.0	3033	3	US-07-325-695-5	Sequence 5, Appl	1351	59	4.9	630	4	US-09-252-991A-31264	Sequence 31264, A
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1280	59	4.9	146	4	US-09-489-039A-9967	Sequence 9967, Ap	1353	59	4.9	661	4	US-09-575-081B-23	Sequence 23, Appl
1281	59	4.9	157	4	US-09-543-681A-7518	Sequence 7518, Ap	1354	59	4.9	674	1	US-08-803-973-7	Sequence 7, Appl
1282	59	4.9	175	2	US-08-408-095-14	Sequence 14, Appl	1355	59	4.9	674	1	US-08-803-972-7	Sequence 7, Appl
1283	59	4.9	177	4	US-09-492-308A-22	Sequence 22, Appl	1356	59	4.9	680	4	US-09-270-767-43944	Sequence 43944, A
1284	59	4.9	177	4	US-09-492-308A-22	Sequence 22, Appl	1357	59	4.9	707	1	US-08-803-973-12	Sequence 12, Appl
1285	59	4.9	181	4	US-09-252-991A-26970	Sequence 26970, A	1358	59	4.9	707	1	US-08-803-972-12	Sequence 12, Appl
1286	59	4.9	181	4	US-09-492-308A-2	Sequence 2, Appl	1359	59	4.9	714	2	US-08-990-114-3	Sequence 3, Appl
1287	59	4.9	196	4	US-09-248-796A-17445	Sequence 17445, A	1360	59	4.9	714	2	US-08-990-114-3	Sequence 3, Appl
1288	59	4.9	202	3	US-08-134-001C-3396	Sequence 3396, Ap	1361	59	4.9	735	4	US-09-241-333-3	Sequence 3, Appl
1289	59	4.9	218	4	US-09-328-352-6389	Sequence 6389, Ap	1362	59	4.9	735	4	US-09-270-767-40232	Sequence 40232, A
1290	59	4.9	225	4	US-09-107-532A-4826	Sequence 4826, Ap	1363	59	4.9	783	6	US-09-270-767-55448	Sequence 55448, A
1291	59	4.9	231	4	US-09-270-767-31808	Sequence 31808, A	1364	59	4.9	826	3	US-09-564-805-2	Sequence 2, Appl
1292	59	4.9	231	4	US-09-270-767-47025	Sequence 47025, A	1365	59	4.9	833	4	US-09-543-681A-4884	Sequence 4884, Ap
1293	59	4.9	294	4	US-09-583-110-3740	Sequence 3740, Ap	1366	59	4.9	936	4	US-09-252-991A-30190	Sequence 30190, A
1294	59	4.9	294	4	US-09-270-767-45782	Sequence 45782, A	1367	59	4.9	1036	4	US-09-328-352-5723	Sequence 5723, Ap
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1296	59	4.9	334	4	US-09-270-767-45533	Sequence 45533, A	1369	59	4.9	1207	4	US-08-158-232-43	Sequence 43, Appl
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1303	59	4.9	355	4	US-08-461-244-2	Sequence 2, Appl	1376	59	4.9	1220	4	US-09-715-962-4	Sequence 4, Appl
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1305	59	4.9	355	4	US-09-534-185-56	Sequence 56, Appl	1378	59	4.9	1353	3	US-08-894-173-2	Sequence 2, Appl
1306	59	4.9	367	4	US-09-464-035A-9	Sequence 9, Appl	1379	59	4.9	1353	3	US-09-398-193-2	Sequence 2, Appl
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1317	59	4.9	409	1	US-08-440-210-21	Sequence 21, Appl	1390	59	4.9	1480	1	US-08-136-742A-2	Sequence 2, Appl
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1331	59	4.9	489	1	US-08-589-893-12	Sequence 12, Appl	1404	59	4.9	1480	3	US-09-425-453A-2	Sequence 2, Appl
1332	59	4.9	489	2	US-09-062-890-12	Sequence 12, Appl	1405	59	4.9	1480	4	US-09-425-453A-4	Sequence 4, Appl
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1417 59 4.9 1480 5 PCT-US93-11667-2 Sequence 2, Appl
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1419 59 4.9 2749 4 US-09-385-222A-4 Sequence 4, Appl
1420 58.5 4.9 61 4 US-09-621-976-4504 Sequence 4504, Ap
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1422 58.5 4.9 102 1 US-08-409-373B-2 Sequence 2, Appl
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1426 58.5 4.9 145 4 US-09-270-767-39754 Sequence 39754, A
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1436 58.5 4.9 210 2 US-08-726-136-1 Sequence 1, Appl
1437 58.5 4.9 210 3 US-09-103-434-1 Sequence 1, Appl
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1441 58.5 4.9 232 4 US-09-540-236-3177 Sequence 3956, Ap
1442 58.5 4.9 232 4 US-09-583-110-3956 Sequence 94, Appl
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1456 58.5 4.9 320 4 US-09-520-781-81 Sequence 4355, Ap
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1458 58.5 4.9 364 4 US-09-270-767-57702 Sequence 2008, Ap
1459 58.5 4.9 367 4 US-09-540-236-2008 Sequence 2, Appl
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1475 58.5 4.9 450 4 US-09-270-767-42412 Sequence 5465, Ap
1476 58.5 4.9 457 4 US-09-107-532A-5465 Sequence 19135, A
1477 58.5 4.9 465 4 US-09-252-991A-19135 Sequence 16, Appl
1478 58.5 4.9 475 4 US-09-627-650B-16 Sequence 16, Appl
1479 58.5 4.9 475 3 US-09-436-063C-16 Sequence 31, Appl
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1484 58.5 4.9 479 4 US-09-198-452A-763 Sequence 14, Appl
1485 58.5 4.9 487 4 US-09-627-650B-14 Sequence 14, Appl
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1490 58.5 4.9 506 4 US-09-436-063C-15 Sequence 15, Appl
1491 58.5 4.9 510 3 US-08-508-761B-4 Sequence 4, Appl
1492 58.5 4.9 521 4 US-09-710-279-532 Sequence 532, App
1493 58.5 4.9 525 3 US-09-134-001C-3514 Sequence 3514, Ap
1494 58.5 4.9 533 4 US-09-672-494-2 Sequence 2, Appl
1495 58.5 4.9 548 4 US-09-328-352-6605 Sequence 6605, Ap
1496 58.5 4.9 560 3 US-09-134-001C-4343 Sequence 4343, Ap
1497 58.5 4.9 599 4 US-09-328-352-4814 Sequence 4814, Ap
1498 58.5 4.9 607 1 US-07-959-943-7 Sequence 7, Appl
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ALIGNMENTS

RESULT 1

US-08-691-814B-6

Sequence 6, Application US/08691814B

Patent No. 5981218

GENERAL INFORMATION:

APPLICANT: Rio, Marie-Christine

APPLICANT: Tomasetto, Catherine

APPLICANT: Basset, Paul

APPLICANT: Byrne, Jennifer

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful

TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave, NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/691,814B

FILING DATE: 31-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,183

FILING DATE: 09-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1383.0090001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-691-814B-6

Query Match 55.6%; Score 664; DB 2; Length 445;

Best Local Similarity 56.2%; Pred. No. 7e-68;

Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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RESULT 2
US-08-846-762-92
; Sequence 92, Application US/08846762A
; Patent No. 5994072
; GENERAL INFORMATION:
; APPLICANT: Lam, Joseph S.
; APPLICANT: Burrows, Lori
; APPLICANT: Charter, Deborah
; APPLICANT: de Kievit, Teresa
; TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
; TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
; FILE REFERENCE: 6580-089
; CURRENT APPLICATION NUMBER: US/08/846,762A
; CURRENT FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 92
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

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Best Local Similarity 24.0%; Pred. No. 0.57;
Matches 31; Conservative 20; Mismatches 51; Indels 27; Gaps 4;

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Qy 167 ETWFLDFKV 175
Db 326 PLLYIDYDKL 334

RESULT 3
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; Sequence 9711, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9711
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9711

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Best Local Similarity 31.8%; Pred. No. 1;

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Qy 164 AWIETW 169
Db 141 SWLPSY 146

RESULT 4
US-09-171-699-4
; Sequence 4, Application US/09171699
; Patent No. 6448389
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy & Biology
; APPLICANT: Gonczol, Eva
; APPLICANT: Berencsi, Klara
; APPLICANT: Karl, Csaba
; TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/171,699
; FILING DATE: 19-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 60/015,717
; APPLICATION DATE: 23-APR-1996
; FILING DATE: 23-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST66APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4

Query Match 6.7%; Score 79.5; DB 4; Length 406;
Best Local Similarity 19.3%; Pred. No. 1.6;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

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Db 227 LSCVLEETSV-----MLAKRPLITKPEVISVMKRIEELCMKVFQO-----YILGADPLR 277

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Db 321 SPVPATIPLSVIVAENSQDESEQSDDEE 350

RESULT 5
PCT-US94-02107-2
; Sequence 2, Application PC/TUS9402107
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy and Biology
; TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02107
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/017,130
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST6BPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-02107-2

Query Match 6.7%; Score 79.5; DB 5; Length 406;
Best Local Similarity 19.3%; Pred. No. 1.6;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSSSHASLNINHSINTQLMARIESY-----EGREKKGISDVRRTCLFVTFDLPVTL 68
Db 142 GCSQAALQNLPCQSDPEIMAYQAQKIFKILDEERDK-----VLTHIDHIFMDI 190
QY 69 LWIIELVNNGGIENTLEKEVMQYDY-----YSSYFDIFLLAVFRFKVLLIAYAVCRL 120
Db 191 L-----TTCVETMCNEYKVTSDACMWTMYGGLISLSEF-----CRV 226
QY 121 RHWMAIALTTAVTSAPFLAK-----VILSKLFSQAGFYVL----- 156
Db 227 LSCVLEETSV-----MLAKPLITKPEVISVMKRIEEICMKVFAQ-----YILGADPLR 277

QY 157 ---PIISFILAWIETWFLDPKVLPOEAEEENRLLIVODASERAAALIPGGISDGOFYSPPE 213
Db 278 VCSPSVD-----DLRAIAEESDEBEAIVAYTLATR-----GASSSDSLVSPPE 320
QY 214 S-----EAGSEAEKQDSEK 229

Db 321 SPVPATIPLSVIVAENSQDESEQSDDEE 350

RESULT 6
US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 503
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2246292CDI
US-09-976-594-503

Query Match 6.7%; Score 79.5; DB 4; Length 723;
Best Local Similarity 18.0%; Pred. No. 3.7;
Matches 34; Conservative 40; Mismatches 58; Indels 57; Gaps 8;

QY 58 FVTFDLPVTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLI----- 112
Db 13 FMSVDICVTTAIVF-----SHLDRSLLEDIRHFNIFDSVLDLMAACLYRSCLLLGATIG 67
QY 113 ----LAVAVCRLR-HWMAIALTTAVTSAPFLAKVILSKLFSQ-----GAGFY 154
Db 68 VAKNSALGPRRLRASLWLVSLVCLFVGIYAVKLL-----LFSEVRRPDRDPWFNLFVWTY 124
QY 155 VLPIISFILAWIETWFLDPKVLPOEAEEENRLLIVODASERAAALIPGGLSDGOFY----- 209
Db 125 ISLGASFLWL-----LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

QY 210 SPPESEAGS 218
Db 164 PPPEQASGA 172

RESULT 7
US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 41033
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033

Query Match 6.6%; Score 78.5; DB 4; Length 221;
Best Local Similarity 22.5%; Pred. No. 0.9;
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;

QY 56 CLFVTFDL-----LFVTLWIIELNVNNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLI 112

Db 17 CIVIYSSMDQFLFIILLILLTCLSFVEXYLFVNLIXIDNYGNXNVFLFLLFXII 76
QY 113 LAYAVCLRHWAIALTT-AVTSAFILAKVILKLSQAGFYVL-PIISFILAWIETW 169
Db 77 VVYFCCSCTTYQLIQCTYNSINFRNLKNLSUT-----LGLISPPLSIHFSYLPY 129
QY 170 FLDPKVLPOAEENRLL-----IVQDASERAAL--IPGGLSDQGF 208
Db 130 LVNNSVLHLKNVXIQEFLDXVVKCFPFLIRASFRCLOIPNGL--GQF 176
RESULT 8
US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56249
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249
Query Match 6.6%; Score 78.5; DB 4; Length 221;
Best Local Similarity 22.5%; Pred. No. 0.9;
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;
QY 56 CLFVTFDL----LFVTLMIELNVNGGIENTLEKEVQYDYSSYDFIFLLAVFRKVL 112
Db 17 CIVIYSSMDQFLFIILLILLTCLSFVEXYLFVNLIXIDNYGNXNVFLFLLFXII 76
QY 113 LAYAVCLRHWAIALTT-AVTSAFILAKVILKLSQAGFYVL-PIISFILAWIETW 169
Db 77 VVYFCCSCTTYQLIQCTYNSINFRNLKNLSUT-----LGLISPPLSIHFSYLPY 129
QY 170 FLDPKVLPOAEENRLL-----IVQDASERAAL--IPGGLSDQGF 208
Db 130 LVNNSVLHLKNVXIQEFLDXVVKCFPFLIRASFRCLOIPNGL--GQF 176
RESULT 9
US-09-248-796A-20444
; Sequence 20444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20444
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20444
Query Match 6.5%; Score 78; DB 4; Length 228;
Best Local Similarity 22.1%; Pred. No. 1.1;

Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;
QY 63 LLFVTL-----LWIIELNVN---GGIENTLEKEVQYDYSSYF-----DIFLLAVF 106
Db 91 LVFTALTSYGAFWLSFAAINIPTFGILAAAYQKDMTQLSSALAFYLIWAILSFIFMLLTF 150
QY 107 RKVLLILAYAVCLRHWAIALTTAVTSAFILAKVILKLSQAGFYVLPIISF----- 161
Db 151 KSTVLLSGFFLC-----LTALFSLLSASYFVGSVALTK--AAGAFGVIAVVAALYDTFA 202
QY 162 ILAWIETWELDFKVLPL---OEAEEE 183
Db 203 LLATKONSFTPLVPLPGSEAKQE 227
RESULT 10
US-09-270-767-43373
; Sequence 43373, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43373
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43373
Query Match 6.5%; Score 78; DB 4; Length 251;
Best Local Similarity 18.8%; Pred. No. 1.2;
Matches 34; Conservative 46; Mismatches 63; Indels 38; Gaps 6;
QY 5 PEDMENAL--TGSQSHASLRNIHSINPTLMARIESYEGREKKIGSDVRETCFLVTFD 62
Db 51 PDSADNAVIESGIQSLNDVQGLN--RPTDLSLAE-----KPDADRPKTGTIDAF 103
QY 63 LLFVTLMIELNVNGGIENTLEKEVQYDYSSYDFIFLLAVFRKVLILAYAVCLRH 122
Db 104 TASISVILLTELG-----DKTFIAIMAMRHPRLIVFGGAIA--- 141
QY 123 WWAIALTTAVTSAFILAKVILKLSQAGFYVLPIISFILAWIETWFLDKVLPOAE 182
Db 142 --ALALMTILSCAFGMAANFIPKIYT-----YYISTALFLIFGLKMLYDGYKMKPTDAQ 194
QY 183 E 183
Db 195 E 195
RESULT 11
US-08-833-752-9
; Sequence 9, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

```

; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6692938e
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-938-719-9

Query Match 6.5%; Score 78; DB 4; Length 355;
Best Local Similarity 23.2%; Pred. No. 2;
Matches 39; Conservative 25; Mismatches 60; Indels 44; Gaps 7

QY 62 DLLFVTLL--WI-IELNVNGGIENTLEKEVMQYDY---YSSYDFIFLLAVRFKVLILAY 115
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
DB 80 DLLFIFLTPWIDYKLDKDDWVFGDAMCKIISGFYTTGLYSEIFFILLTIDRYLAIVHAV 139
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 116 AVCRLRH-----WVAIALTTAVTSAFL-----LAKVILSK 145
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
DB 140 FAIRARTVTGCVITSIIIWAIIASIMPLGYFSKTQWEFTHTCSLHPHESLREWKLFQ 199
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 146 LFSQAGFYVLPPIISFLIAWIEFWLDFKVLPOEAREN-----RLIV 169
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
DB 200 ALKLNLFGLVPLLVMIICYIGI----IKILLRPNEKKSKAVALIFV 243
||||| :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

RESULT 13
US-08-466-103A-14
; Sequence 14, Application US/08466103A
; Patent No. 5856124
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
; APPLICANT: Ebisawa, Takashi
; TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,103A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/319,887
; FILING DATE: 07-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,857
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/250002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; FRAGMENT TYPE: internal
US-08-466-103A-14
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 2.6;
Matches 29; Conservative 20; Mismatches 38; Indels 44; Gaps 4;

Qy 63 LLEFVTLMIIEIENVNGGIENTLEKEVMQYD--YYSYFDFLLAVFRFKVLLIAYAVCRL 120
Db 148 LCYVFLIWMULTI---AIMPNTQGTQYDPRIYSCTF----- 182

Qy 121 RHWAIATLTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLDFKVLPOEA 180
Db 183 -----TQSVSSAYTIAVV-----FHFIIVPMIIVFCYLRIRIWLVLQVRRVK 225

Qy 181 EENRLLIVOD 191
Db 226 PDNKPCLKPQD 236

RESULT 14
US-09-280-420-2
; Sequence 2, Application US/09280420
; Patent No. 6037131
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
; TITLE OF INVENTION: MELATONIN 1A RECEPTOR GENE
; FILE REFERENCE: 10217/727002
; CURRENT FILING DATE: 2000-01-07
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: US 60/053,565
; PRIOR APPLICATION NUMBER: 1997-07-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-09-479-195-2

Query Match 6.4%; Score 77; DB 3; Length 353;
Best Local Similarity 22.1%; Pred. No. 2.6;
Matches 29; Conservative 20; Mismatches 38; Indels 44; Gaps 4;

Qy 63 LLEFVTLMIIEIENVNGGIENTLEKEVMQYD--YYSYFDFLLAVFRFKVLLIAYAVCRL 120
Db 148 LCYVFLIWMULTI---AIMPNTQGTQYDPRIYSCTF----- 182

Qy 121 RHWAIATLTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLDFKVLPOEA 180
Db 183 -----TQSVSSAYTIAVV-----FHFIIVPMIIVFCYLRIRIWLVLQVRRVK 225

Qy 181 EENRLLIVOD 191
Db 226 PDNKPCLKPQD 236

Search completed: January 24, 2005, 16:13:50
Job time : 55 secs

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GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: January 24, 2005, 16:12:47 ; Search time 157 Seconds
 (without alignments)
 534.667 Million cell updates/sec

Title: US-10-063-518-14
 Perfect score: 1195
 Sequence: 1 MNHLPEMENALTGSQSSHA.....EAGSEAEKQDSKPLLEL 234
 Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2002273
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Database :
 Listing first 1500 summaries
 1: A_Geneseq_23Sep04:*
 2: Genesecp1980s:*
 3: Genesecp1990s:*
 4: Genesecp2000s:*
 5: Genesecp2001s:*
 6: Genesecp2002s:*
 7: Genesecp2003as:*
 8: Genesecp2003Bs:*
 9: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29056	standard; protein; 234 AA.				
DE	Human PRO polypeptide sequence #33.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 2						
ID	AAM39929	standard; protein; 234 AA.				
DE	Human polypeptide SEQ ID NO 3074.					
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSRQ INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 3						
ID	AAB87532	standard; protein; 234 AA.				
DE	Human PRO1864.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 4						
ID	ABG95857	standard; protein; 234 AA.				
DE	Human secreted/transmembrane protein PRO1864.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 5;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 5						
ID	ABB4847	standard; protein; 234 AA.				
DE	Human PRO1864 protein sequence SEQ ID NO:62.					
PN	WO20020690-A2.					
PD	03-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 5;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 6						
ID	ABB95453	standard; protein; 234 AA.				

DE Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 Query Match 100.0%; Score 1195; DB 5; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 7
 ID ABUS8432 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 8
 ID ABU87980 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 9
 ID ABU84295 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 10
 ID ABR66169 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 11
 ID ABR65559 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 12
 ID ABU99499 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 13
 ID ABU82738 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 RESULT 14
 ID ABU89859 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.

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PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 15
ID ABR68108 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 16
ID ABU96161 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 17
ID ABU92592 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 18
ID ABO08669 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 19
ID ABO02721 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 20
ID ABR74875 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 21
ID ABR94637 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 22
ID ABU85610 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 23
ID ABR98770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 24
ID ABR97985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 25
ID ABU91691 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 26
ID ABU89384 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 27
ID ABU86225 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 28
ID ABU67438 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 29
ID ABU80466 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 30
ID ABU90882 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 31
ID ABO33941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 32
ID ABR99384 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 33
ID ABR98774 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 34
ID ABO16297 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.

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PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 35
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 36
ID ABO18838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 38
ID ABR39937 standard; protein; 234 AA.
DE Human prostate selective polypeptide Pr340.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 39
ID ABR71958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 40
ID ABU84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 41
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 43
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 44
ID ABU98685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 45
ID ABU83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 52
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 54
ID ABU71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003013855-A1.
PD 16-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 55
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 59
ID ABO15687 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 60
ID ABU55968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 61
ID ABU7293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 62
ID ABU65296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 63
ID ABU95241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003036143-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 66
ID ABR69995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 69
ID ABU81271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BCU0092 protein #SEQ ID 20.
PN WQ2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 72
ID ABU90966 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027268-A1.

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PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 75
ID ABR68413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 77
ID ABR8305 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 78
ID ABU89995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 79
ID ABU83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 80
ID ABU94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 81
ID ABU90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 82
ID ABU83990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 83
ID ABU93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 84
ID ABR64886 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 85
ID ABO27287 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 87
ID ABO6534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 89
ID ABU56963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 90
ID ABU85915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 91
ID ABU82202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 92
ID ABU87213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 93
ID ABU83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 94
ID ABO8059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

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RESULT 95
ID ABU92482 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 96
ID ABU81770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 97
ID ABU65934 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 98
ID ABU81152 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 99
ID ABR59763 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 100
ID ABU93951 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 101
ID ABU99804 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 102
ID ABR66474 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 103
ID ABR90892 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 104
ID ABO53267 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 105
ID ABU94319 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 106
ID ABU79201 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 107
ID ABU86530 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 108
ID ABU86835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 109
ID ABU94624 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 110
ID ABO4551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 111
ID ABR70300 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 112
ID ABU98465 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 113
ID ABR65864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 114
ID ABR64581 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 115
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ID ABU79506 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 116
ID ABU92897 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 117
ID ABU95856 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 118
ID ABU91076 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 119
ID ABU90169 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 120
ID ABO9584 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 121
ID ABO10856 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 122
ID ABR70910 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 123
ID ABU98269 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 124
ID ABU87518 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 125
ID ABU91886 standard; protein; 234 AA.
DE Human PRO polypeptide #33.

PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 126
ID ABU9274 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 127
ID ABU84600 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 128
ID ABR69690 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 129
ID ABU80067 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 130
ID ABU82481 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 131
ID ABU93336 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 132
ID ABO9889 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 133
ID ABO8974 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 134
ID ABU96445 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 135
ID ABU10542 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.

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PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 136
ID ABR80849 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 146
ID ABR81154 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 147
ID ABR80850 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 148
ID ABR88452 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 149
ID ABR77273 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 150
ID ABO28757 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 151
ID ABO31502 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 152
ID ABR7919 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 153
ID ABO40399 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 154
ID ABO35824 standard; protein; 234 AA.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 137
ID ABR72115 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 137
ID ABR95551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 138
ID ABR96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 139
ID ABR70605 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 140
ID ABO04956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 141
ID ABO08364 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 142
ID ABO05571 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 143
ID ABR73960 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 144
ID ABR95552 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 145
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DE Human PRO polypeptide #33.
PN US2003068701-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 155
ID ABO43963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 156
ID ADA77818 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 157
ID ABM24758 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 158
ID ABO03026 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 159
ID ABR90282 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 160
ID ABM17196 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 161
ID ABR94942 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 162
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 163
ID ADB17071 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 164
ID ABO21485 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 165
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 166
ID ABR87537 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 167
ID ABM77578 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 168
ID ABM27808 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 169
ID ABM06089 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 170
ID ABM03595 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 171
ID ABM35046 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 172
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 173
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 183
ID ABM09444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 184
ID ABO41314 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 185
ID ABO36123 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 186
ID ABO43658 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 187
ID ABM76358 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 188
ID ABM76054 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 189
ID ABM25673 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 190
ID ABM25978 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 191
ID ASO03331 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 192
ID ASO03331 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 192
ID ABO02416 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 193
ID ABO44245 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 194
ID ABR90587 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 195
ID ABR73655 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 196
ID ABO16907 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 197
ID ABR94332 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 198
ID ABR75839 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 199
ID ABR71215 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 200
ID ABR93112 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 201
ID ABR93417 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054478-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 202
ID ABR87842 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 203
ID ABO27842 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 204
ID ABO29977 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 205
ID ABO33186 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 206
ID ABO4874 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 207
ID ABO8834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 208
ID ABO36434 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 209
ID ABO35519 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 210
ID ABO39484 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068776-A1.
PD 10-APR-2003.

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RESULT 229
ID ABM35351 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 230
ID ABM33114 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 231
ID ABO52640 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 232
ID ABO50200 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 233
ID ABU99194 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 234
ID ABO4246 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 235
ID ABO5876 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 236
ID ABM18416 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 237
ID ABR97444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 238
ID ABR80544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 239
ID ABM01155 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 240
ID ABR88757 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 241
ID ABM13409 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 242
ID ABM20793 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 243
ID ABO41924 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 244
ID ABO42534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 245
ID ABM10054 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 246
ID ABO38569 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 247
ID ABM32809 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 248
ID ABM22623 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 249
ID ABM74834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 250
ID ADA79610 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 251
ID ABR96224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 252
ID ABM02375 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 253
ID ABR86317 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 254
ID ABR8622 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 255
ID ABM16586 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 256
ID ABM29638 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 257
ID ABO29062 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068693-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 258
ID ABM23843 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 259
ID ABM23233 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 260
ID ABM22013 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 261
ID ABO37654 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 262
ID ABM28418 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 263
ID ABM28723 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 264
ID ABM66367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 265
ID ABM75749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 266
ID ABM34029 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 267
ID AEM34334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 271
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003052222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 275
ID ABR99689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 276
ID ABR00545 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 277
ID ASM00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 278
ID ABO29672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 279
ID AEM23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 280
ID AEM29333 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003088679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 282
ID ABO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 283
ID ABO20488 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 286
ID ABO18228 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 287
ID ABO22655 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 288
ID ABO22960 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 289
ID ABR92502 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 290
ID ABR81459 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 291
ID ABR77883 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 292
ID ABR89672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 293
ID ABR26588 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 294
ID ABR13714 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 295
ID ABO28452 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.

PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 296
ID ABO30282 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 297
ID ABR07309 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 298
ID ABR01900 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 299
ID ABO37044 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 300
ID ABO41619 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 301
ID ABO35214 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 302
ID ABR25063 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 303
ID ABO47455 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 304
ID ABO47760 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049747-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 314

ID ABM12189 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003084445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003086896-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 318
ID ABM04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 319
ID ABM06699 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 320
ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 323
ID ABM25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104541-A1.

PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 324
ID ABM19878 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 325
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 326
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 327
ID ADA89135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 328
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 329
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 330
ID ABR98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 331
ID ABO06839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 332
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 333
ID ABR7350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 334
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 335
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 336
ID ABM18111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 337
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 338
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 339
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 340
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 341
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 342
ID ABM1274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

ID ABO37959 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 354
ID ABM66672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 355
ID ADR20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 356
ID ABM19573 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 359
ID ADA78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 360
ID ABR88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.

PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 362
ID ABM26893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 363
ID ABM03290 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 364
ID ABO39789 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 365
ID ABO49895 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 366
ID ABO50810 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 367
ID ABO05266 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 368
ID ABR74570 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 369
ID ABR77049 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 370
ID ABM17806 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 371
ID ABR95857 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 372
ID ABO21790 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 373
ID ABO19960 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 374
ID ABO24263 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 375
ID ABR86012 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 376
ID ABM10664 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 377
ID ABM76663 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 378
ID ABR89367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 379
ID ABM12494 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 380
ID ABM05784 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068717-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 381
ID ABO34909 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 382
ID ABO2985 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 383
ID ABO1963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 384
ID ABO19268 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 385
ID ABO4679 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 386
ID ABO4980 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 387
ID ABR69023 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 388
ID ABR9062 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 389
ID ABR72435 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 390
ID ABR74265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 391
ID ABO19533 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 392
ID ABR80239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 393
ID ABO1460 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 394
ID ABO2070 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 395
ID ABR87232 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003086687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 396
ID ABO12799 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 397
ID ABO30553 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 398
ID ABO24453 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 399
ID ABO29367 standard; protein; 234 AA.

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DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 400
ID ABO31197 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 401
ID ABM14324 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 402
ID ABM09749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 403
ID ABO38874 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 404
ID ABM34639 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 405
ID ABO51115 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 406
ID ABO03941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 407
ID ABO10411 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 408
ID ABR77654 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 409
ID ABR7864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 410
ID ABO23958 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 411
ID ABR93722 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 412
ID ABM01765 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 413
ID ABM78188 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 414
ID ABR89977 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 415
ID ABM27503 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 416
ID ABM13104 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 417
ID ABO31807 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 418

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ID ABM14019 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 419
ID ABM08224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 420
ID ABO40094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 421
ID ABM74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 422
ID ABM33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 423
ID ABM20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 424
ID ABO48675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 425
ID ABR72740 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 426
ID ABO15382 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 427
ID ABR85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040065-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 429
ID ABO17212 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 430
ID ABM17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 431
ID ABR85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 432
ID ABM76968 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003084459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 434
ID ABM22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 435
ID ABM30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 436
ID ABM21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
Pred. No. 1.3e-131;
RESULT 437
ID ABR85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040065-A1.
PD 27-FEB-2003.

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DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 438
ID ABM14934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 439
ID ABO41009 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 440
ID ABO36739 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 441
ID ABO37349 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 442
ID ABM75139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 443
ID ABM33419 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 444
ID ABO46174 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 445
ID ADA82501 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 446
ID ADB85587 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 447
ID ABM31773 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 448
ID ABM31163 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 449
ID ADB85809 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 450
ID ABM32078 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 451
ID ABM32383 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 452
ID ADB68266 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 453
ID ADB68073 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 454
ID ABM31468 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 455
ID ABM30858 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068771-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 456
ID ADB90890 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 457
ID ADC06970 standard; protein; 234 AA.
DE Human secreted protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 458
ID ADC17149 standard; protein; 234 AA.
DE Mammalian PRO polypeptide (SeqID 14).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 459
ID ADC14847 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 460
ID ADCS2342 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 462
ID ADD10351 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 463
ID ADD11311 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 464
ID ADD37104 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 465
ID ADD36018 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 466
ID ADG01019 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 467
ID ADG08572 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 468
ID ADG02534 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 469
ID ADG01241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 470
ID ADF95416 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 471
ID ADF95193 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 472
ID ADG12331 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 473
ID ADH24046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

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RESULT 474
ID ADH34072 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 475
ID ADH29905 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 476
ID ADH23876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 477
ID ADH08891 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 478
ID ADH85280 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 479
ID ADH24556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 480
ID ADH37412 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 481
ID ADH02001 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 482
ID ADH37582 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 483
ID ADH53491 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 484
ID ADH24216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 485
ID ADH38510 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 486
ID ADG83631 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 487
ID ADH29439 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 488
ID ADH27555 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 489
ID ADH37752 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 490
ID ADH37929 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 491
ID ADH57349 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 492
ID ADH53491 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

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DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181636-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 493
ID ADH53661 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 494
ID ADH51997 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 495
ID ADH49852 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 496
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 497
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 498
ID ADI25332 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 499
ID ADH97706 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 500
ID ADI03554 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 501
ID ADI11911 standard; protein; 234 AA.
DE Human PRO polypeptide #7.

PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 502
ID ADH89985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 503
ID ADH98386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 504
ID ADI11061 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 505
ID ADI11571 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 506
ID ADH98216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 507
ID ADH98556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 508
ID ADH98046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 509
ID ADI05034 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 510
ID ADI03384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181654-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 511
ID ADI04779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 513
ID ADI19577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 515
ID ADI03044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 518
ID ADI01261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 519
ID ADI01956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 520
ID ADI03214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 521
ID ADI11401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 522
ID ADI02303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 523
ID ADI11741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 524
ID ADI05378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 526
ID ADI19407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 527
ID ADI05208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 529
ID ADI01446 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 530
ID ADI01616 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 531
ID ADI01786 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 532
ID ADH79790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 533
ID ADI04608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 534
ID ADI02744 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 535
ID ADH78063 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 536
ID ADI25702 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 537
ID ADI25872 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 538
ID ADK65384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 539
ID ADH98726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 540
ID ADH79967 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 541
ID ADL32672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 542
ID ADM30206 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 543
ID ADL93698 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 544
ID ADC52152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 545
ID ADE41312 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 546
ID ADE74203 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 547

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ID ADE74815 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 548
ID ADF96028 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 549
ID ADO4299 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 550
ID ADG0459 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 551
ID ADH06584 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 552
ID ADH06414 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 553
ID ADG6835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 554
ID ADH27725 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 555
ID ADH25066 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 556
ID ADH33698 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181645-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 557
ID ADG82715 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 558
ID ADH02341 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 559
ID ADH07948 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 560
ID ADG69345 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 561
ID ADH39166 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 562
ID ADH25996 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 563
ID ADG83906 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 564
ID ADG85450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 565
ID ADH06244 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180854-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 566
ID ADH310074 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 567
ID ADH24386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 568
ID ADH32965 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 569
ID ADG69515 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 570
ID ADH07778 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 571
ID ADG85790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 572
ID ADH39336 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 573
ID ADH33528 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 574
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 575
ID ADH01078 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 576
ID ADG69685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 577
ID ADH02171 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 578
ID ADG69175 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 579
ID ADG85960 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 580
ID ADH24896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 581
ID ADH39513 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 582
ID ADH02511 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 583
ID ADG69005 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 584
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 584
ID ADH07608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 585
ID ADG86130 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 586
ID ADH24726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 587
ID ADH25774 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 588
ID ADH38340 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 589
ID ADH57179 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 590
ID ADH43495 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 591
ID ADH52167 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 592
ID ADH49533 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 593
ID ADH90495 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 594
ID ADI11231 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 595
ID ADH98896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 596
ID ADI02126 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 597
ID ADH90665 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 598
ID ADJ54704 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 599
ID ADJ98540 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 600
ID ADJ98710 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 601
ID ADH78869 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 602
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ID ADJ99103 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 603
ID ADJ99273 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 604
ID ADJ98891 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 605
ID ADH79039 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 606
ID ADK08099 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 607
ID ADK14420 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 608
ID ADK82840 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 609
ID ADJ64475 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 610
ID ADM31371 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 611
ID ADM36418 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 612
ID ADM40223 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 613
ID ADM80869 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 614
ID ADL91873 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:94.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 615
ID ADN37831 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 616
ID AAM41716 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6647.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 617
ID AAM41715 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6646.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 618
ID ABP75508 standard; protein; 238 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 692.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 1195; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 619
ID ABR58404 standard; protein; 234 AA.
DE Human NOV19b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.4%; Score 1188; DB 6; Length 234;
Best Local Similarity 99.6%; Pred. No. 8.5e-131;
RESULT 620
ID AAM39930 standard; protein; 216 AA.
DE Human polypeptide SEQ ID NO 3075.

PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 91.8%; Score 1097; DB 4; Length 216;
Best Local Similarity 92.3%; Pred. No. 3.9e-120;
RESULT 621
ID ABB90287 standard; protein; 201 AA.
DE Human polypeptide SEQ ID NO 2663.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 85.7%; Score 1024; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
RESULT 622
ID ABR58403 standard; protein; 198 AA.
DE Human NOV19a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 82.4%; Score 985; DB 6; Length 198;
Best Local Similarity 84.6%; Pred. No. 5.1e-107;
RESULT 623
ID AAU30250 standard; protein; 283 AA.
DE Novel human secreted protein #741.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.0%; Score 777; DB 4; Length 283;
Best Local Similarity 72.5%; Pred. No. 2.5e-82;
RESULT 624
ID ADS64413 standard; protein; 176 AA.
DE Human protein encoded by clone FEERA20007820.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 56.0%; Score 669.5; DB 7; Length 176;
Best Local Similarity 87.5%; Pred. No. 5.7e-70;
RESULT 625
ID ADK36828 standard; protein; 146 AA.
DE Novel human polypeptide SeqID8910.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 55.6%; Score 665; DB 5; Length 146;
Best Local Similarity 91.0%; Pred. No. 1.5e-69;
RESULT 626
ID AAU25768 standard; protein; 445 AA.
DE Human MLN 64.
PN WO9706256-A2.
PD 20-FEB-1997.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CENT NAT RECH SCI.
PA (UYPA-) UNIV PASTEUR LOUIS.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.1e-69;
RESULT 627
ID ABR47530 standard; protein; 445 AA.
DE Breast cancer associated protein sequence SEQ ID NO:296.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 55.6%; Score 664; DB 6; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.1e-69;
RESULT 628
ID ADH13184 standard; protein; 445 AA.
DE Human malignant neoplasia-related protein SeqID33.
PN EPI365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 55.6%; Score 664; DB 8; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.1e-69;

RESULT 629
ID ABG05498 standard; protein; 534 AA.
DE Novel human diagnostic protein #5489.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.3%; Score 625; DB 4; Length 534;
Best Local Similarity 48.9%; Pred. No. 4.6e-64;
RESULT 630
ID ABR69622 standard; protein; 412 AA.
DE Human CGDP-22 protein.
PN WO2003027263-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 48.4%; Score 578; DB 6; Length 412;
Best Local Similarity 58.3%; Pred. No. 1.1e-58;
RESULT 631
ID ABP75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 33.9%; Score 405.5; DB 6; Length 111;
Best Local Similarity 73.7%; Pred. No. 3.4e-39;
RESULT 632
ID ABB59968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 28.7%; Score 343; DB 4; Length 580;
Best Local Similarity 37.8%; Pred. No. 7.6e-31;
RESULT 633
ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.9%; Score 322; DB 4; Length 70;
Best Local Similarity 98.4%; Pred. No. 1.2e-29;
RESULT 634
ID AAB96837 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST PR RECH EXPL MER.
Query Match 7.8%; Score 93.5; DB 4; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.11;
RESULT 635
ID AAU03699 standard; protein; 373 AA.
DE Group B Streptococcus antigenic protein, ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 7.6%; Score 91; DB 4; Length 373;
Best Local Similarity 25.7%; Pred. No. 0.18;
RESULT 636
ID ABP30317 standard; protein; 651 AA.
DE Streptococcus polypeptide SEQ ID NO 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 651;
Best Local Similarity 25.7%; Pred. No. 0.4;
RESULT 637
ID ABP29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.4;
RESULT 638
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.4;
RESULT 639
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.14;
RESULT 640
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.14;
RESULT 641
ID AAB58945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 87.5; DB 3; Length 516;
Best Local Similarity 25.2%; Pred. No. 0.74;
RESULT 642
ID ADE28099 standard; protein; 340 AA.
DE Human NTPAN protein - SEQ ID 4.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 85.5; DB 7; Length 340;
Best Local Similarity 25.5%; Pred. No. 0.71;
RESULT 643
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 396;
Best Local Similarity 21.0%; Pred. No. 0.88;
RESULT 644
ID AAW13575 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1;
RESULT 645
ID AAW13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1;
RESULT 646
ID AAW13582 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L46.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.

PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1;
RESULT 647
ID AAW13577 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L39.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1;
RESULT 648
ID ADA05822 standard; protein; 440 AA.
DE Human NOV43a protein SEQ ID NO:182.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 85.5; DB 6; Length 440;
Best Local Similarity 25.2%; Pred. No. 1;
RESULT 649
ID ADN63244 standard; protein; 440 AA.
DE Human NOV43a variant.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT-) SMITHSON G.
PA (MILL-) MILLET I.
PA (PEYM-) PEYMAN J A.
PA (KEKU-) KEKUDA R.
PA (JULJ-) JU J.
PA (LILL-) LI L.
PA (GUOX-) GUO X.
PA (PATT-) PATTURAJAN M.
PA (SPYT-) SPYTEK K A.
PA (EDIN-) EDINGER S R.
PA (ELLE-) ELLERMAN K.
PA (MALY-) MALYANKAR U M.
PA (ORTT-) ORT T.
PA (GORM-) GORMAN L.
PA (ZERH-) ZERHUSEN B D.
PA (ANDE-) ANDERSON D W.
PA (ZHON-) ZHONG M.
PA (CATT-) CATTERTON E.
PA (JIWW-) JI W.
PA (MILL-) MILLER C E.
PA (RAST-) RASTELLI L.
PA (STON-) STONE D J.
PA (PENA-) PENA C E A.
PA (SHEN-) SHENOY S G.
PA (SHIM-) SHIMKETS R A.
PA (ROTH-) ROTHENBERG M E.
PA (LEAC-) LEACH M D.
PA (AGEE-) AGEE M L.
PA (BERG-) BERGHS C.
PA (DIPL-) DIPIPO V A.
PA (EISE-) EISEN A.
PA (GANG-) GANGOLI E A.
PA (RIEG-) RIEGER D K.
PA (SPAD-) SPADERNA S K.
Query Match 7.2%; Score 85.5; DB 8; Length 440;
Best Local Similarity 25.2%; Pred. No. 1;
RESULT 650
ID ADN62985 standard; protein; 440 AA.
DE Human NOV43a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT-) SMITHSON G.
PA (MILL-) MILLET I.
PA (PEYM-) PEYMAN J A.
PA (KEKU-) KEKUDA R.
PA (JULJ-) JU J.
PA (LILL-) LI L.
PA (GUOX-) GUO X.

PA (PATV/) PATTURAJAN M.
PA (SPYT/) SPYTEK K. A.
PA (EDIN/) EDINGER S. R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U. M.
PA (ORTT/) ORT. T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B. D.
PA (ANDE/) ANDERSON D. W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI. W.
PA (MILL/) MILLER C. E.
PA (RASI/) RASTELLI L.
PA (STON/) STONE D. J.
PA (PENA/) PENNA C. E. A.
PA (SHEN/) SHENOY S. G.
PA (SHIM/) SHIMKETS R. A.
PA (ROTH/) ROTHENBERG M. E.
PA (LEAC/) LEACH M. D.
PA (AGEE/) AGEE M. L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V. A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E. A.
PA (RIEG/) RIEGER D. K.
PA (SPAD/) SPADERNA S. K.
Query Match
Best Local Similarity 25.2%; DB 8; Length 440;
Score 85.5; DB 8; Length 440;
Pred. No. 1;
RESULT 651
ID AAW13593 standard; protein; 467 AA.
DE Batten disease CLN3 mutant protein in family L61.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO/) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match
Best Local Similarity 25.5%; DB 2; Length 467;
Score 85.5; DB 2; Length 467;
Pred. No. 1.1;
RESULT 652
ID ABB89640 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 2016.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 25.2%; DB 5; Length 473;
Score 85.5; DB 5; Length 473;
Pred. No. 1.1;
RESULT 653
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 25.2%; DB 8; Length 473;
Score 85.5; DB 8; Length 473;
Pred. No. 1.1;
RESULT 654
ID ABU40544 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #26071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 26.0%; DB 6; Length 500;
Score 85.5; DB 6; Length 500;
Pred. No. 1.2;
RESULT 655
ID ABU33210 standard; protein; 430 AA.
DE Protein encoded by Prokaryotic essential gene #18737.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 25.5%; DB 6; Length 430;
Score 84.5; DB 6; Length 430;
Pred. No. 1.3;
RESULT 656
ID AAW13588 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L10.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO/) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match
Best Local Similarity 24.8%; DB 2; Length 438;
Score 84.5; DB 2; Length 438;
Pred. No. 1.3;
RESULT 657
ID AAG16921 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 33.7%; DB 3; Length 322;
Score 83.5; DB 3; Length 322;
Pred. No. 1.1;
RESULT 658
ID ABG21285 standard; protein; 472 AA.
DE Novel human diagnostic protein #21276.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.1%; DB 4; Length 472;
Score 83.5; DB 4; Length 472;
Pred. No. 1.9;
RESULT 659
ID ABU35608 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21135.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.7%; DB 6; Length 239;
Score 82.5; DB 6; Length 239;
Pred. No. 0.99;
RESULT 660
ID AAW13590 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L216.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO/) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match
Best Local Similarity 24.8%; DB 2; Length 438;
Score 82.5; DB 2; Length 438;
Pred. No. 2.3;
RESULT 661
ID ADB85263 standard; protein; 589 AA.
DE Mouse RNAI homologue SEQ ID NO:144.
PN EPI284297-A2.
PD 19-FEB-2003.
PA (WARN-) WARNER LAMBERT CO.
Query Match
Best Local Similarity 19.5%; DB 7; Length 589;
Score 82; DB 7; Length 589;
Pred. No. 3.9;
RESULT 662
ID AAW13586 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L285.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO/) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match
Best Local Similarity 24.8%; DB 2; Length 438;
Score 81.5; DB 2; Length 438;
Pred. No. 3;
RESULT 663
ID AAB92924 standard; protein; 519 AA.
DE Human protein sequence SEQ ID NO:11574.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 22.6%; DB 4; Length 519;
Score 81.5; DB 4; Length 519;
Pred. No. 3.8;
RESULT 664
ID ADE28193 standard; protein; 577 AA.
DE Human MDDT protein - SEQ ID 43.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.6%; DB 7; Length 577;
Score 81.5; DB 7; Length 577;
Pred. No. 4.4;
RESULT 665
ID AAG53771 standard; protein; 322 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.6;
RESULT 666
ID AAG25639 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.6;
RESULT 667
ID AAG53746 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.6;
RESULT 668
ID ABO63194 standard; protein; 350 AA.
DE Klebsiella pneumoniae polypeptide seqid 9711.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.7%; Score 80.5; DB 7; Length 350;
Best Local Similarity 31.8%; Pred. No. 2.9;
RESULT 669
ID ABB48552 standard; protein; 463 AA.
DE Listeria monocytogenes protein #1256.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.7%; Score 80.5; DB 5; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.2;
RESULT 670
ID ABU33036 standard; protein; 463 AA.
DE Protein encoded by Prokaryotic essential gene #18563.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 80.5; DB 6; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.2;
RESULT 671
ID ADD43870 standard; protein; 536 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 165.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 6.7%; Score 80.5; DB 7; Length 536;
Best Local Similarity 25.2%; Pred. No. 5.2;
RESULT 672
ID ADC42920 standard; protein; 891 AA.
DE Vaccinia Virus Major Core protein P4a precursor.
PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.7%; Score 80.5; DB 7; Length 891;
Best Local Similarity 23.3%; Pred. No. 11;
RESULT 673
ID ABB92830 standard; protein; 1780 AA.
DE Herbicidially active polypeptide SEQ ID NO 2041.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 80.5; DB 5; Length 1780;
Best Local Similarity 20.8%; Pred. No. 27;
RESULT 674
ID AAB54399 standard; protein; 144 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 6.7%; Score 80; DB 3; Length 144;
Best Local Similarity 25.4%; Pred. No. 0.96;
RESULT 675
ID AAM39952 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 3097.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 238;
Best Local Similarity 22.5%; Pred. No. 1.9;
RESULT 676
ID ADM04473 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:3158.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 80; DB 7; Length 238;
Best Local Similarity 22.5%; Pred. No. 1.9;
RESULT 677
ID AAM41738 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 6669.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 249;
Best Local Similarity 22.5%; Pred. No. 2.1;
RESULT 678
ID AAR77844 standard; protein; 309 AA.
DE Molasses toxicity resistance protein RTM1.
PN WO9514774-A2.
PD 01-JUN-1995.
PA (CNRS) CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 2; Length 309;
Best Local Similarity 28.0%; Pred. No. 2.8;
RESULT 679
ID ASB67388 standard; protein; 330 AA.
DE Photorhabdus luminescens protein sequence #485.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 6; Length 330;
Best Local Similarity 24.6%; Pred. No. 3;
RESULT 680
ID AAE03831 standard; protein; 360 AA.
DE Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 4; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.4;
RESULT 681
ID ASB64559 standard; protein; 360 AA.
DE Human albumin fusion protein #1234.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 5; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.4;
RESULT 682
ID ADL77826 standard; protein; 360 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1308.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.7%; Score 80; DB 8; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.4;
RESULT 683
ID ABU25554 standard; protein; 365 AA.
DE Protein encoded by Prokaryotic essential gene #11081.
PN WO200277183-A2.
PD 03-OCT-2002.

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PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.7%; Score 79.5; DB 6; Length 365;
 Best Local Similarity 21.2%; Pred. No. 4;
 RESULT 684
 ID AAR58703 standard; protein; 406 AA.
 DE HCMV IE-exon-4 subunit.
 PN WO9417810-A1.
 PD 18-AUG-1994.
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 Query Match 6.7%; Score 79.5; DB 2; Length 406;
 Best Local Similarity 19.3%; Pred. No. 4.6;
 RESULT 685
 ID AAW27775 standard; protein; 406 AA.
 DE Human cytomegalovirus immediate-early exon 4 product.
 PN WO9740165-A1.
 PD 30-OCT-1997.
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 Query Match 6.7%; Score 79.5; DB 2; Length 406;
 Best Local Similarity 19.3%; Pred. No. 4.6;
 RESULT 686
 ID ABE58483 standard; protein; 638 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 2241.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.7%; Score 79.5; DB 4; Length 638;
 Best Local Similarity 20.5%; Pred. No. 8.7;
 RESULT 687
 ID AAE13277 standard; protein; 723 AA.
 DE Human transporters and ion channels (TRICH)-4.
 PN WO200177174-A2.
 PD 18-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.7%; Score 79.5; DB 5; Length 723;
 Best Local Similarity 18.0%; Pred. No. 10;
 RESULT 688
 ID ADL12774 standard; protein; 723 AA.
 DE Human steroid-induced C3A liver cell protein #80.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 6.7%; Score 79.5; DB 8; Length 723;
 Best Local Similarity 18.0%; Pred. No. 10;
 RESULT 689
 ID AAW20696 standard; protein; 121 AA.
 DE H. pylori secreted or periplasmic protein 05ae20220orf50.
 PN WO9640893-A1.
 PD 19-DEC-1996.
 PA (ASTR) ASTRA AB.
 Query Match 6.6%; Score 79; DB 2; Length 121;
 Best Local Similarity 21.4%; Pred. No. 0.99;
 RESULT 690
 ID ABB60462 standard; protein; 323 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.6%; Score 79; DB 4; Length 323;
 Best Local Similarity 18.8%; Pred. No. 3.9;
 RESULT 691
 ID ABR58610 standard; protein; 1531 AA.
 DE Human cancer related protein SEQ ID NO:267.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 6.6%; Score 79; DB 6; Length 1531;
 Best Local Similarity 24.3%; Pred. No. 33;
 RESULT 692
 ID ADE31753 standard; protein; 1531 AA.
 DE Human 59590 protein #SEQ ID 110.
 PN WO2003065984-A2.
 PD 14-AUG-2003.
 PA (MILL-) MILLENNIUM PHARM INC.

Query Match 6.6%; Score 79; DB 7; Length 1531;
 Best Local Similarity 24.3%; Pred. No. 33;
 RESULT 693
 ID ABUE2069 standard; protein; 1597 AA.
 DE Human heart alpha-kinase (HK).
 PN US2002177205-A1.
 PD 28-NOV-2002.
 PA (RYAZ/) RYAZANOV A.
 Query Match 6.6%; Score 79; DB 6; Length 1597;
 Best Local Similarity 24.3%; Pred. No. 35;
 RESULT 694
 ID ABUE2070 standard; protein; 1597 AA.
 DE Mouse heart alpha-kinase (HK).
 PN US2002177205-A1.
 PD 28-NOV-2002.
 PA (RYAZ/) RYAZANOV A.
 Query Match 6.6%; Score 79; DB 6; Length 1597;
 Best Local Similarity 24.3%; Pred. No. 35;
 RESULT 695
 ID ABO55689 standard; protein; 135 AA.
 DE Human genome derived single exon protein #1923.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 6.6%; Score 78.5; DB 8; Length 135;
 Best Local Similarity 59.4%; Pred. No. 1.3;
 RESULT 696
 ID ADB10816 standard; protein; 228 AA.
 DE Alloiococcus otitis antigenic protein SEQ ID NO:4244.
 PN WO2003048304-A2.
 PD 12-JUN-2003.
 PA (AMHP) WYETH HOLDINGS CORP.
 Query Match 6.6%; Score 78.5; DB 6; Length 228;
 Best Local Similarity 22.5%; Pred. No. 2.7;
 RESULT 697
 ID ABU36298 standard; protein; 239 AA.
 DE Protein encoded by Prokaryotic essential gene #21825.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.6%; Score 78.5; DB 6; Length 239;
 Best Local Similarity 23.4%; Pred. No. 2.9;
 RESULT 698
 ID ADJ27174 standard; protein; 626 AA.
 DE Human TRICH-6, SEQ ID 6.
 PN WO2004013293-A2.
 PD 12-FEB-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 6.6%; Score 78.5; DB 8; Length 626;
 Best Local Similarity 18.0%; Pred. No. 11;
 RESULT 699
 ID ABP29904 standard; protein; 669 AA.
 DE Streptococcus polypeptide SEQ ID NO 8984.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 6.6%; Score 78.5; DB 5; Length 669;
 Best Local Similarity 23.5%; Pred. No. 12;
 RESULT 700
 ID ABP28724 standard; protein; 669 AA.
 DE Streptococcus polypeptide SEQ ID NO 6624.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 6.6%; Score 78.5; DB 5; Length 669;
 Best Local Similarity 23.5%; Pred. No. 12;
 RESULT 701
 ID ADI21047 standard; protein; 703 AA.
 DE Novel human protein #22.

PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 78.5; DB 7; Length 703;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 702
ID ABP52105 standard; protein; 723 AA.
DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.6%; Score 78.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 703
ID AAE02437 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 704
ID AAE02441 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 705
ID AAE02442 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 706
ID AAG67163 standard; protein; 766 AA.
DE Amino acid sequence of a human 33894 transporter polypeptide.
PN WO200164875-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 707
ID AAG79246 standard; protein; 766 AA.
DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN WO200173018-A2.
PD 04-OCT-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 708
ID ABB98345 standard; protein; 766 AA.
DE Human ABC transporter ABCB9 SEQ ID NO. 6.
PN WO200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 709
ID AAE21170 standard; protein; 766 AA.
DE Human TRICH-14 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 710
ID AAG20805 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN EP1033405-A2.
Query Match 6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 23.8%; Pred. No. 6.3;
RESULT 711
ID AAG20804 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 442;
Best Local Similarity 23.8%; Pred. No. 7.8;
RESULT 712
ID AAU35545 standard; protein; 471 AA.
DE Haemophilus influenzae cellular proliferation protein #186.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 4; Length 471;
Best Local Similarity 25.0%; Pred. No. 8.6;
RESULT 713
ID ABU30411 standard; protein; 471 AA.
DE Protein encoded by Prokaryotic essential gene #15938.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 6; Length 471;
Best Local Similarity 25.0%; Pred. No. 8.6;
RESULT 714
ID AAG20803 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 489;
Best Local Similarity 23.8%; Pred. No. 9;
RESULT 715
ID ABB49039 standard; protein; 269 AA.
DE Listeria monocytogenes protein #1743.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 6.5%; Score 77.5; DB 5; Length 269;
Best Local Similarity 22.0%; Pred. No. 4.5;
RESULT 716
ID AEG17374 standard; protein; 280 AA.
DE Novel human diagnostic protein #17365.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 4; Length 280;
Best Local Similarity 21.9%; Pred. No. 4.8;
RESULT 717
ID ABO00771 standard; protein; 280 AA.
DE Polypeptide encoded by novel human contig #22.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 4.8;
RESULT 718
ID ABU48889 standard; protein; 327 AA.
DE Protein encoded by Prokaryotic essential gene #34416.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 77.5; DB 6; Length 327;
Best Local Similarity 24.8%; Pred. No. 5.9;
RESULT 719
ID AAU1576 standard; protein; 438 AA.
DE Mouse Batten disease polypeptide CLN3 homologue.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 5.9;

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Best Local Similarity 27.6%; Pred. No. 8.9;
RESULT 720
ID ADC42919 standard; protein; 892 AA.
DE Variola smallpox virus A10L.
PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.5%; Score 77.5; DB 7; Length 892;
Best Local Similarity 22.7%; Pred. No. 24;
RESULT 721
ID AAR88413 standard; protein; 353 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.5;
RESULT 722
ID AAW23958 standard; protein; 353 AA.
DE Mouse melatonin 1a receptor.
PN WO9803549-A1.
PD 29-JAN-1998.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.5;
RESULT 723
ID ABB07571 standard; protein; 353 AA.
DE Mouse melatonin 1a (Mella) receptor.
PN US6326526-B1.
PD 04-DEC-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.4%; Score 77; DB 5; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.5;
RESULT 724
ID ADO29553 standard; protein; 353 AA.
DE Mouse GPCR MTR1A, SEQ ID NO:655.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.4%; Score 77; DB 8; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.5;
RESULT 725
ID ADM25403 standard; protein; 383 AA.
DE Hyperthermophile Methanopyrus kandleri protein #9.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 6.4%; Score 77; DB 7; Length 383;
Best Local Similarity 24.8%; Pred. No. 8.4;
RESULT 726
ID AAG42521 standard; protein; 648 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 648;
Best Local Similarity 20.4%; Pred. No. 17;
RESULT 727
ID ABUL16172 standard; protein; 650 AA.
DE Protein encoded by Prokaryotic essential gene #1699.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 728
ID ABM72713 standard; protein; 650 AA.
DE Staphylococcus aureus protein #1953.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 22.5%; Pred. No. 1.1e+02;

Best Local Similarity 27.5%; Pred. No. 18;
RESULT 729
ID AAG42520 standard; protein; 690 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 690;
Best Local Similarity 20.4%; Pred. No. 19;
RESULT 730
ID AAG42519 standard; protein; 728 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 728;
Best Local Similarity 20.4%; Pred. No. 21;
RESULT 731
ID AAG32549 standard; protein; 805 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 24;
RESULT 732
ID AAG32548 standard; protein; 847 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 847;
Best Local Similarity 20.4%; Pred. No. 25;
RESULT 733
ID AAG32547 standard; protein; 991 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 991;
Best Local Similarity 20.4%; Pred. No. 31;
RESULT 734
ID ABP52133 standard; protein; 1025 AA.
DE Plasmodium falciparum multidrug resistance protein SEQ ID NO:85.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.4%; Score 77; DB 5; Length 1025;
Best Local Similarity 20.6%; Pred. No. 33;
RESULT 735
ID AAG42381 standard; protein; 1047 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1047;
Best Local Similarity 20.4%; Pred. No. 34;
RESULT 736
ID AAG42380 standard; protein; 1191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1191;
Best Local Similarity 20.4%; Pred. No. 41;
RESULT 737
ID AAG42379 standard; protein; 1202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1202;
Best Local Similarity 20.4%; Pred. No. 41;
RESULT 738
ID AAR29527 standard; protein; 2510 AA.
DE HCV antigen T7N1-30.
PN EP518313-A2.
PD 16-DEC-1992.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 6.4%; Score 77; DB 2; Length 2510;
Best Local Similarity 22.5%; Pred. No. 1.1e+02;
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RESULT 739
ID ADF74966 standard; protein; 249 AA.
DE Human 164-1b protein (SeqID 25).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 249;
Best Local Similarity 23.3%; Pred. No. 5.3;
RESULT 740
ID ADC01137 standard; protein; 278 AA.
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 6.4%; Score 76.5; DB 7; Length 278;
Best Local Similarity 28.5%; Pred. No. 6.2;
RESULT 741
ID ABO65827 standard; protein; 435 AA.
DE Klebsiella pneumoniae polypeptide seqid 12344.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 76.5; DB 7; Length 435;
Best Local Similarity 21.8%; Pred. No. 12;
RESULT 742
ID ADF74969 standard; protein; 481 AA.
DE Human 164-1b protein (SeqID 28).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 13;
RESULT 743
ID AAR90765 standard; protein; 494 AA.
DE Human K+ channel 2 mature protein.
PN WO9603415-A1.
PD 08-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 744
ID AAW42996 standard; protein; 494 AA.
DE Putative mature potassium channel 2 protein.
PN US5710019-A.
PD 20-JAN-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 745
ID ABP58356 standard; protein; 494 AA.
DE Human potassium channel subunit Kv5.1.
PN WO200296944-A2.
PD 05-DEC-2002.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.4%; Score 76.5; DB 6; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 746
ID ADC99155 standard; protein; 494 AA.
DE Human mature K+ channel 2 protein.
PN US2003092895-A1.
PD 15-MAY-2003.
PA (LIYY/) LI Y.
PA (ADAM/) ADAMS M D.
PA (WHIT/) WHITE O R.
Query Match 6.4%; Score 76.5; DB 7; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 747
ID AAW20085 standard; protein; 509 AA.
DE Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 509;
Best Local Similarity 22.0%; Pred. No. 19;
RESULT 748
ID ADB63857 standard; protein; 555 AA.
DE Human protein encoded by clone ASTR020053430.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 76.5; DB 7; Length 555;
Best Local Similarity 23.3%; Pred. No. 16;
RESULT 749
ID ABB08159 standard; protein; 570 AA.
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN WO200242330-A2.
PD 30-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 76.5; DB 5; Length 570;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 750
ID AAW20918 standard; protein; 593 AA.
DE H. pylori transporter protein, 149p12015orf14.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 593;
Best Local Similarity 19.2%; Pred. No. 18;
RESULT 751
ID ADN46225 standard; protein; 615 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.4%; Score 76.5; DB 8; Length 615;
Best Local Similarity 22.6%; Pred. No. 19;
RESULT 752
ID ADH88107 standard; protein; 195 AA.
DE Enterococcus faecalis polypeptide #2587.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.4%; Score 76; DB 7; Length 195;
Best Local Similarity 25.9%; Pred. No. 4.3;
RESULT 753
ID AAG09592 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 274;
Best Local Similarity 26.7%; Pred. No. 6.9;
RESULT 754
ID AAG09591 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 287;
Best Local Similarity 26.7%; Pred. No. 7.4;
RESULT 755
ID ABB89424 standard; protein; 456 AA.
DE Human polypeptide SEQ ID NO 1800.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 5; Length 456;
Best Local Similarity 22.0%; Pred. No. 14;
RESULT 756
ID AAB53400 standard; protein; 557 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO: 940.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 3; Length 557;
Best Local Similarity 22.0%; Pred. No. 19;

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RESULT 757
ID AAY4945 standard; protein; 593 AA.
DE Wheat sulphate permease-2.
PN WO200004154-A2.
PD 27-JAN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.4%; Score 76; DB 3; Length 593;
Best Local Similarity 21.4%; Pred. No. 20;
RESULT 758
ID ABB63150 standard; protein; 228 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16242.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (SEKE) PE CORP NY.
Query Match 6.3%; Score 75.5; DB 4; Length 228;
Best Local Similarity 21.8%; Pred. No. 6.2;
RESULT 759
ID ADK46633 standard; protein; 263 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3148.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75.5; DB 8; Length 263;
Best Local Similarity 18.0%; Pred. No. 7.5;
RESULT 760
ID ADM92206 standard; protein; 263 AA.
DE S. pneumoniae antigenic protein sequence SeqID403.
PN WO2004020609-A2.
PD 11-MAR-2004.
PA (TUFT) UNIV TUFTS.
Query Match 6.3%; Score 75.5; DB 8; Length 263;
Best Local Similarity 18.0%; Pred. No. 7.5;
RESULT 761
ID AAY81619 standard; protein; 264 AA.
DE Streptococcus pneumoniae type 4 protein sequence #119.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MTCR-) MICROBIAL TECHNIQUES LTD.
Query Match 6.3%; Score 75.5; DB 3; Length 264;
Best Local Similarity 18.0%; Pred. No. 7.5;
RESULT 762
ID ABU02182 standard; protein; 276 AA.
DE S. pneumoniae type 4 strain protein from coding region #1759.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.3%; Score 75.5; DB 6; Length 276;
Best Local Similarity 18.0%; Pred. No. 8;
RESULT 763
ID ABG93285 standard; protein; 342 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 538.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.3%; Score 75.5; DB 5; Length 342;
Best Local Similarity 21.9%; Pred. No. 11;
RESULT 764
ID AAB15936 standard; protein; 352 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:293.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 75.5; DB 3; Length 352;
Best Local Similarity 31.7%; Pred. No. 11;
RESULT 765
ID ADH51470 standard; protein; 363 AA.
DE Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN FR2835847-A1.
PD 15-AUG-2003.
PA (SERV-) LES LAB SERVIER SA.
Query Match 6.3%; Score 75.5; DB 7; Length 363;
Best Local Similarity 23.5%; Pred. No. 12;

RESULT 766
ID AAU03851 standard; protein; 397 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 397;
Best Local Similarity 19.1%; Pred. No. 13;
RESULT 767
ID AAU03852 standard; protein; 433 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 433;
Best Local Similarity 19.1%; Pred. No. 15;
RESULT 768
ID ADO29507 standard; protein; 471 AA.
DE Mouse GPCR HTR2A, SEQ ID NO:609.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.3%; Score 75.5; DB 8; Length 471;
Best Local Similarity 21.0%; Pred. No. 17;
RESULT 769
ID AAU03820 standard; protein; 499 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 499;
Best Local Similarity 19.1%; Pred. No. 18;
RESULT 770
ID ADM72132 standard; protein; 392 AA.
DE Human NTRAN polypeptide (clone ID 7524555CD1).
PN WO2004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 392;
Best Local Similarity 21.0%; Pred. No. 15;
RESULT 771
ID AAU45917 standard; protein; 445 AA.
DE Propionibacterium acnes immunogenic protein #6813.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 4; Length 445;
Best Local Similarity 24.8%; Pred. No. 18;
RESULT 772
ID ABM42436 standard; protein; 445 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 6; Length 445;
Best Local Similarity 24.8%; Pred. No. 18;
RESULT 773
ID ADA34178 standard; protein; 467 AA.
DE Acinetobacter baumannii protein #1339.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75; DB 6; Length 467;
Best Local Similarity 23.1%; Pred. No. 19;
RESULT 774
ID ADP99138 standard; protein; 480 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN WO2004048599-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 480;
Best Local Similarity 21.0%; Pred. No. 20;
RESULT 775

ID ADH6490 standard; protein; 549 AA.
 DE Enterococcus faecalis polypeptide #970.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 6.3%; Score 75; DB 7; Length 549;
 Best Local Similarity 18.7%; Pred. No. 24;
 RESULT 776
 ID AAR54066 standard; protein; 1051 AA.
 DE Non-A, non-B hepatitis virus gene #4 product.
 PN JP6141870-A.
 PD 24-MAY-1994.
 PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
 PA (SANW) SANWA KAGAKU KENKYUSHO CO.
 PA (TOFU) TONEN CORP.
 Query Match 6.3%; Score 75; DB 2; Length 1051;
 Best Local Similarity 23.4%; Pred. No. 59;
 RESULT 777
 ID AAR9361 standard; protein; 1051 AA.
 DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
 PN JP07133291-A.
 PD 23-MAY-1995.
 PA (TOFU) TONEN CORP.
 Query Match 6.3%; Score 75; DB 2; Length 1051;
 Best Local Similarity 23.4%; Pred. No. 59;
 RESULT 778
 ID ADB64712 standard; protein; 1131 AA.
 DE Human protein encoded by clone NT2NE20077270.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.3%; Score 75; DB 7; Length 1131;
 Best Local Similarity 23.9%; Pred. No. 65;
 RESULT 779
 ID ABB64494 standard; protein; 2248 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 20274.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.3%; Score 75; DB 4; Length 2248;
 Best Local Similarity 22.9%; Pred. No. 1.7e+02;
 RESULT 780
 ID ADG20763 standard; protein; 2248 AA.
 DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.
 PN WO2003103704-A2.
 PD 18-DEC-2003.
 PA (DEVE-) DEVELOPMENTAL BIOLOGICALS CORP.
 Query Match 6.3%; Score 75; DB 8; Length 2248;
 Best Local Similarity 22.9%; Pred. No. 1.7e+02;
 RESULT 781
 ID AAB66797 standard; protein; 200 AA.
 DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.
 PN WO200102858-A1.
 PD 11-JAN-2001.
 PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
 PA (MATE-) INST MATERIALS RES & ENG.
 Query Match 6.2%; Score 74.5; DB 4; Length 200;
 Best Local Similarity 23.8%; Pred. No. 6.7;
 RESULT 782
 ID ADF74954 standard; protein; 256 AA.
 DE Rat 164-1h protein (SeqID 13).
 PN WO2003097686-A1.
 PD 27-NOV-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 6.2%; Score 74.5; DB 8; Length 256;
 Best Local Similarity 23.3%; Pred. No. 9.5;
 RESULT 783
 ID AAR53748 standard; protein; 355 AA.
 DE Seven transmembrane receptor (V28).
 PN WO9412635-A2.
 PD 09-JUN-1994.
 PA (ICOS-) ICOS CORP.
 Query Match 6.2%; Score 74.5; DB 2; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 784
 ID AAW48722 standard; protein; 355 AA.
 DE Human V28 seven transmembrane receptor.
 PN US5759804-A.
 PD 02-JUN-1998.
 PA (ICOS-) ICOS CORP.
 Query Match 6.2%; Score 74.5; DB 2; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 785
 ID AAY90677 standard; protein; 355 AA.
 DE Human mutant G protein-coupled receptor V28 (I230K).
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match 6.2%; Score 74.5; DB 3; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 786
 ID AAY90642 standard; protein; 355 AA.
 DE Human G protein-coupled receptor V28.
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match 6.2%; Score 74.5; DB 3; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 787
 ID AAB21693 standard; protein; 355 AA.
 DE Human 7TM receptor V28 cDNA clone protein #2.
 PN US6107475-A.
 PD 22-AUG-2000.
 PA (ICOS-) ICOS CORP.
 Query Match 6.2%; Score 74.5; DB 3; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 788
 ID AAB21692 standard; protein; 355 AA.
 DE Human 7TM receptor V28 cDNA clone protein #1.
 PN US6107475-A.
 PD 22-AUG-2000.
 PA (ICOS-) ICOS CORP.
 Query Match 6.2%; Score 74.5; DB 3; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 789
 ID AAG80126 standard; protein; 355 AA.
 DE Human CX3CR1 protein.
 PN WO200172830-A2.
 PD 04-OCT-2001.
 PA (IPFP-) IPF PHARM GMBH.
 PA (FORS/) FORSMANN U.
 Query Match 6.2%; Score 74.5; DB 4; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 790
 ID AAB82786 standard; protein; 355 AA.
 DE Human CX3C chemokine receptor 1.
 PN WO200160406-A1.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (NOUN) UNIV NORTHWESTERN.
 Query Match 6.2%; Score 74.5; DB 4; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 791
 ID AAU91235 standard; protein; 355 AA.
 DE Human 7 transmembrane domain receptor V28 #2.
 PN US6348574-B1.
 PD 19-FEB-2002.
 PA (ICOS-) ICOS CORP.
 Query Match 6.2%; Score 74.5; DB 5; Length 355;
 Best Local Similarity 25.8%; Pred. No. 15;
 RESULT 792
 ID AAU91234 standard; protein; 355 AA.
 DE Human 7 transmembrane domain receptor V28 #1.
 PN US6348574-B1.

DE	Human serotonin V28.
PN	US2003105292-A1.
PD	05-JUN-2003.
PA	(LIAM/) LIAN C W.
PA	(BEHA/) BEHAN D P.
PA	(CHAL/) CHALMERS D T.
Query Match	6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity	25.8%; Pred. No. 15;
RESULT 802	
ID	ADH10680 standard; protein; 355 AA.
DE	Human CX3CR1 polypeptide.
PN	WO2003104484-A1.
PD	18-DEC-2003.
PA	(META-) METABOLEX INC.
Query Match	6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity	25.8%; Pred. No. 15;
RESULT 803	
ID	ADO29269 standard; protein; 355 AA.
DE	Human GPCR CX3CR1, SEQ ID NO:370.
PN	WO2004040000-A2.
PD	13-MAY-2004.
PA	(PRIM-) PRIMAL INC.
Query Match	6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity	25.8%; Pred. No. 15;
RESULT 804	
ID	ADQ18141 standard; protein; 355 AA.
DE	Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN	WO2004048938-A2.
PD	10-JUN-2004.
PA	(PROT-) PROTEIN DESIGN LABS INC.
Query Match	6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity	25.8%; Pred. No. 15;
RESULT 805	
ID	AAW77109 standard; protein; 471 AA.
DE	Rat 5-HT2A serotonin receptor C322K mutant.
PN	WO9838217-A1.
PD	03-SEP-1998.
PA	(TEIT/) TEITLER M.
PA	(HERR/) HERRICK-DAVIS K.
PA	(EGAN/) EGAN C C.
Query Match	6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity	21.0%; Pred. No. 22;
RESULT 806	
ID	AAW77111 standard; protein; 471 AA.
DE	Rat 5-HT2A serotonin receptor C322E mutant.
PN	WO9838217-A1.
PD	03-SEP-1998.
PA	(TEIT/) TEITLER M.
PA	(HERR/) HERRICK-DAVIS K.
PA	(EGAN/) EGAN C C.
Query Match	6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity	21.0%; Pred. No. 22;
RESULT 807	
ID	AAW77110 standard; protein; 471 AA.
DE	Rat 5-HT2A serotonin receptor C322R mutant.
PN	WO9838217-A1.
PD	03-SEP-1998.
PA	(TEIT/) TEITLER M.
PA	(HERR/) HERRICK-DAVIS K.
PA	(EGAN/) EGAN C C.
Query Match	6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity	21.0%; Pred. No. 22;
RESULT 808	
ID	AAW77104 standard; protein; 471 AA.
DE	Rat 5-HT2A serotonin receptor.
PN	WO9838217-A1.
PD	03-SEP-1998.
PA	(TEIT/) TEITLER M.
PA	(HERR/) HERRICK-DAVIS K.
PA	(EGAN/) EGAN C C.
Query Match	6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity	21.0%; Pred. No. 22;
RESULT 809	
ID	AAW77104 standard; protein; 471 AA.
DE	Rat 5-HT2A serotonin receptor.
PN	WO9838217-A1.
PD	03-SEP-1998.
PA	(TEIT/) TEITLER M.
PA	(HERR/) HERRICK-DAVIS K.
PA	(EGAN/) EGAN C C.
Query Match	6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity	21.0%; Pred. No. 22;

ID ABB07980 standard; protein; 471 AA.
DE Rat 5-HT2 receptor sequence.
PN US6383762-B1.
PD 07-MAY-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 471;
Best Local Similarity 21.0%; Pred. No. 22;
RESULT 810
ID ADF74971 standard; protein; 481 AA.
DE Rat 164-1b protein (SeqID 30).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 23;
RESULT 811
ID AAM933692 standard; protein; 562 AA.
DE Human polypeptide, SEQ ID NO: 3602.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.2%; Score 74.5; DB 4; Length 562;
Best Local Similarity 23.1%; Pred. No. 28;
RESULT 812
ID ADL31569 standard; protein; 562 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3602.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Score 74.5; DB 8; Length 562;
Best Local Similarity 23.1%; Pred. No. 28;
RESULT 813
ID ABB62948 standard; protein; 597 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 74.5; DB 4; Length 597;
Best Local Similarity 27.2%; Pred. No. 31;
RESULT 814
ID ADA36878 standard; protein; 940 AA.
DE Acinetobacter baumannii protein #4039.
PN US6582958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74.5; DB 6; Length 940;
Best Local Similarity 21.1%; Pred. No. 58;
RESULT 815
ID ABB92731 standard; protein; 1808 AA.
DE Herbicidally active polypeptide SEQ ID NO 1942.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 74.5; DB 5; Length 1808;
Best Local Similarity 17.3%; Pred. No. 1.4e+02;
RESULT 816
ID AAE20477 standard; protein; 3010 AA.
DE HCV-S1 full-length polypeptide.
PN WO200208447-A2.
PD 31-JAN-2002.
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (SHRL/) EHRLICH G.
Query Match 6.2%; Score 74.5; DB 5; Length 3010;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 817
ID ADF07294 standard; protein; 154 AA.
DE Bacterial polypeptide #3407.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74; DB 7; Length 154;
Best Local Similarity 26.4%; Pred. No. 5.4;
RESULT 818

ID ABU70365 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V4.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.4;
RESULT 819
ID ABU70366 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V5.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.4;
RESULT 820
ID ABB54180 standard; protein; 312 AA.
DE Lactococcus lactis protein ylig.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 312;
Best Local Similarity 24.3%; Pred. No. 14;
RESULT 821
ID ABU02869 standard; protein; 324 AA.
DE S. pneumoniae type 4 strain protein from coding region #2450.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.2%; Score 74; DB 6; Length 324;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 822
ID ABO00448 standard; protein; 342 AA.
DE Novel human polypeptide #35.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 74; DB 6; Length 342;
Best Local Similarity 21.2%; Pred. No. 16;
RESULT 823
ID AAR88412 standard; protein; 350 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 17;
RESULT 824
ID AAW15786 standard; protein; 350 AA.
DE Melatonin receptor protein.
PN JP09084581-A.
PD 31-MAR-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 17;
RESULT 825
ID AAW94761 standard; protein; 350 AA.
DE Human melatonin receptor protein mel-1a.
PN EP892046-A2.
PD 20-JAN-1999.
PA (JCRP-) JCR PHARM CO LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 17;
RESULT 826
ID ABP81840 standard; protein; 350 AA.
DE Human melatonin receptor type 1a protein SEQ ID NO:164.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74; DB 6; Length 350;
Best Local Similarity 18.5%; Pred. No. 17;
RESULT 827

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ID ADO2552 standard; protein; 350 AA.
DE Human GPCR MTRIA, SEQ ID NO:154.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC. 6.2%; Score 74; DB 8; Length 350;
Query Match 18.5%; Pred. No. 17;
Best Local Similarity 18.5%; Pred. No. 17;
RESULT 828
ID AAW19220 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9721730-A1.
PD 19-JUN-1997.
PA (MERI-) MERCK & CO INC. 6.2%; Score 74; DB 2; Length 364;
Query Match 19.4%; Pred. No. 18;
Best Local Similarity 19.4%; Pred. No. 18;
RESULT 829
ID ABW73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA. 6.2%; Score 74; DB 6; Length 366;
Query Match 21.8%; Pred. No. 18;
Best Local Similarity 21.8%; Pred. No. 18;
RESULT 830
ID ABE55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yted.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE. 6.2%; Score 74; DB 5; Length 442;
Query Match 20.4%; Pred. No. 23;
Best Local Similarity 20.4%; Pred. No. 23;
RESULT 831
ID AAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAOC) MERCIAN CORP. 6.2%; Score 74; DB 3; Length 492;
Query Match 22.5%; Pred. No. 27;
Best Local Similarity 22.5%; Pred. No. 27;
RESULT 832
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN WO200148216-A1.
PD 05-JUL-2001.
PA (SAOC) MERCIAN CORP. 6.2%; Score 74; DB 4; Length 493;
Query Match 22.5%; Pred. No. 27;
Best Local Similarity 22.5%; Pred. No. 27;
RESULT 833
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOITO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP. 6.2%; Score 74; DB 2; Length 1031;
Query Match 26.2%; Pred. No. 75;
Best Local Similarity 26.2%; Pred. No. 75;
RESULT 834
ID AAR98362 standard; protein; 1031 AA.
DE 5'UTR/CORE/ENV/NS2/NS3 from HCV (#6).
PN JP07133291-A.
PD '23-MAY-1995.
PA (TOFU) TONEN CORP. 6.2%; Score 74; DB 2; Length 1031;
Query Match 26.2%; Pred. No. 75;
Best Local Similarity 26.2%; Pred. No. 75;
RESULT 835
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 120;
Best Local Similarity 20.3%; Pred. No. 4.3;
RESULT 836

ID AAU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN WO200162797-A2.
PD 30-AUG-2001.
PA (PHRA) PHARMACIA & UPJOHN CO. 6.2%; Score 73.5; DB 4; Length 192;
Query Match 26.3%; Pred. No. 8.3;
Best Local Similarity 26.3%; Pred. No. 8.3;
RESULT 837
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 6.2%; Score 73.5; DB 6; Length 268;
Query Match 19.6%; Pred. No. 13;
Best Local Similarity 19.6%; Pred. No. 13;
RESULT 838
ID AAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 282;
Best Local Similarity 28.1%; Pred. No. 14;
RESULT 839
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 6.2%; Score 73.5; DB 7; Length 312;
Query Match 17.4%; Pred. No. 16;
Best Local Similarity 17.4%; Pred. No. 16;
RESULT 840
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 21;
RESULT 841
ID AAG32487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 21;
RESULT 842
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 442;
Best Local Similarity 28.1%; Pred. No. 27;
RESULT 843
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 442;
Best Local Similarity 28.1%; Pred. No. 27;
RESULT 844
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 489;
Best Local Similarity 28.1%; Pred. No. 30;
RESULT 845
ID AAB86544 standard; protein; 491 AA.
DE Human cytomegalovirus strain AD169 IE1 protein.
PN WO200163286-A2.
PD 30-AUG-2001.
PA (KERN/) KERN F. 6.2%; Score 73.5; DB 4; Length 491;
Query Match 19.3%; Pred. No. 31;
Best Local Similarity 19.3%; Pred. No. 31;

RESULT 846
 ID ADP12517 standard; protein; 491 AA.
 DE Protein encoded by mRNA of the invention #127.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 6.2%; Score 73.5; DB 8; Length 491;
 Best Local Similarity 19.3%; Pred. No. 31;
 RESULT 847
 ID ADP12518 standard; protein; 491 AA.
 DE Protein encoded by mRNA of the invention #128.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 6.2%; Score 73.5; DB 8; Length 491;
 Best Local Similarity 19.3%; Pred. No. 31;
 RESULT 848
 ID ADP12513 standard; protein; 491 AA.
 DE Protein encoded by mRNA of the invention #123.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 6.2%; Score 73.5; DB 8; Length 491;
 Best Local Similarity 19.3%; Pred. No. 31;
 RESULT 849
 ID ADP12514 standard; protein; 491 AA.
 DE Protein encoded by mRNA of the invention #124.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 6.2%; Score 73.5; DB 8; Length 491;
 Best Local Similarity 19.3%; Pred. No. 31;
 RESULT 850
 ID ABP73574 standard; protein; 574 AA.
 DE Candida albicans essential protein SEQ ID NO 7411.
 PN WO200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.2%; Score 73.5; DB 5; Length 574;
 Best Local Similarity 20.8%; Pred. No. 38;
 RESULT 851
 ID ABG23128 standard; protein; 682 AA.
 DE Novel human diagnostic protein #29119.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSB-) HYSQ INC.
 Query Match 6.2%; Score 73.5; DB 4; Length 682;
 Best Local Similarity 20.8%; Pred. No. 48;
 RESULT 852
 ID ABB61737 standard; protein; 1287 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PERE-) PE CORP NY.
 Query Match 6.2%; Score 73.5; DB 4; Length 1287;
 Best Local Similarity 18.2%; Pred. No. 1.2e+02;
 RESULT 853
 ID AAR33214 standard; protein; 3033 AA.
 DE NANBH virus strain HC-J8 protein.
 PN EP532167-A2.
 PD 17-MAR-1993.
 PA (IMMO) IMMUNO JAPAN INC.
 Query Match 6.2%; Score 73.5; DB 2; Length 3033;
 Best Local Similarity 27.4%; Pred. No. 3.8e+02;
 RESULT 854
 ID AAW20571 standard; protein; 114 AA.
 DE H. pylori secreted or periplasmic protein 80257.aa.
 PN WO9640893-A1.
 PD 19-DEC-1996.
 PA (ASTR-) ASTRA AB.
 Query Match 6.1%; Score 73; DB 2; Length 114;
 Best Local Similarity 21.6%; Pred. No. 4.6;
 RESULT 855
 ID AAU69567 standard; protein; 189 AA.
 DE Human G protein-coupled receptor from cDNA Seq-2643.
 PN WO200177330-A2.
 PD 18-OCT-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 6.1%; Score 73; DB 5; Length 189;
 Best Local Similarity 20.3%; Pred. No. 9.3;
 RESULT 856
 ID ADC97146 standard; protein; 199 AA.
 DE E. faecium protein sequence SEQ ID 6773.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.1%; Score 73; DB 7; Length 199;
 Best Local Similarity 22.6%; Pred. No. 10;
 RESULT 857
 ID ABP29367 standard; protein; 249 AA.
 DE Streptococcus polypeptide SEQ ID NO 7910.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 6.1%; Score 73; DB 5; Length 249;
 Best Local Similarity 24.6%; Pred. No. 14;
 RESULT 858
 ID AAU87836 standard; protein; 272 AA.
 DE T. aureum 7091 elongase TELO1 from plasmid pRAT-4-A1.
 PN WO200208401-A2.
 PD 31-JAN-2002.
 PA (ABBO) ABBOTT LAB.
 Query Match 6.1%; Score 73; DB 5; Length 272;
 Best Local Similarity 19.9%; Pred. No. 15;
 RESULT 859
 ID ADH80191 standard; protein; 272 AA.
 DE Fungal 7091 elongase protein seq id 75.
 PN US2003163845-A1.
 PD 28-AUG-2003.
 PA (MUKE/) MUKERJI P.
 PA (LEON/) EUN-YEONG LEONARD A.
 PA (HUAN/) HUANG Y.
 PA (PERE/) PEREIRA S L.
 Query Match 6.1%; Score 73; DB 8; Length 272;
 Best Local Similarity 19.9%; Pred. No. 15;
 RESULT 860
 ID ABM73154 standard; protein; 290 AA.
 DE Staphylococcus aureus protein #2394.
 PN WO200294868-A2.
 PD 28-NOV-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 6.1%; Score 73; DB 6; Length 290;
 Best Local Similarity 23.4%; Pred. No. 17;
 RESULT 861
 ID ABR47464 standard; protein; 322 AA.
 DE Breast cancer associated protein sequence SEQ ID NO:160.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 6.1%; Score 73; DB 6; Length 322;
 Best Local Similarity 20.6%; Pred. No. 20;
 RESULT 862
 ID ADN61865 standard; protein; 349 AA.
 DE Human novel protein NOV42a.
 PN US2004043382-A1.
 PD 04-MAR-2004.
 PA (PADI/) PADIGARU M.
 PA (SPYT/) SPYTEK K A.
 PA (SHEN/) SHENOY S G.
 PA (TAUP/) TAUFIER R J.
 PA (PENA/) PENNA C E A.
 PA (LILL/) LI L.
 PA (ZERH/) ZERHUSEN B D.
 PA (GUSE/) GUSEV V Y.
 PA (JIWW/) JI W.

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PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CAIT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 6.1%; Score 73; DB 8; Length 349;
Best Local Similarity 24.0%; Pred. No. 22;
RESULT 863
ID AAW19613 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9722004-A1.
PD 19-JUN-1997.
PA (MERI/) MERCK & CO INC.
Query Match 6.1%; Score 73; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 23;
RESULT 864
ID AAV54565 standard; protein; 364 AA.
DE A mouse growth hormone secretagogue receptor.
PN WO200002919-A1.
PD 20-JAN-2000.
PA (MERI/) MERCK & CO INC.
Query Match 6.1%; Score 73; DB 3; Length 364;
Best Local Similarity 19.4%; Pred. No. 23;
RESULT 865
ID AAB97377 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor (GHSR) related protein.
PN WO200132705-A1.
PD 10-MAY-2001.
PA (TAKE/) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 73; DB 4; Length 364;
Best Local Similarity 19.4%; Pred. No. 23;
RESULT 866
ID ADO29026 standard; protein; 364 AA.
DE Mouse novel GPCR GHSR, SEQ ID NO:125.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM/) PRIMAL INC.
Query Match 6.1%; Score 73; DB 8; Length 364;
Best Local Similarity 19.4%; Pred. No. 23;
RESULT 867
ID AAW77773 standard; protein; 377 AA.
DE Staphylococcus aureus protein of unknown function.
PN EP841394-A2.
PD 13-MAY-1998.
PA (SMIK/) SMITHKLINE BEECHAM CORP.
PA (SMIK/) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 377;
Best Local Similarity 23.3%; Pred. No. 24;
RESULT 868
ID AAG50065 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 415;
Best Local Similarity 19.8%; Pred. No. 28;
RESULT 869

ID AAG24013 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN EP1033405-A2.
Query Match 6.1%; Score 73; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 29;
RESULT 870
ID AAG24012 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 29;
RESULT 871
ID ABU31419 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #16946.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 453;
Best Local Similarity 26.5%; Pred. No. 31;
RESULT 872
ID AAG50064 standard; protein; 472 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 472;
Best Local Similarity 19.8%; Pred. No. 33;
RESULT 873
ID AAG50063 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 474;
Best Local Similarity 19.8%; Pred. No. 33;
RESULT 874
ID ABM70313 standard; protein; 490 AA.
DE Photorhabdus luminescens protein sequence #3410.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 73; DB 6; Length 490;
Best Local Similarity 24.6%; Pred. No. 35;
RESULT 875
ID AAY33766 standard; protein; 495 AA.
DE hkV5.1 human brain-specific potassium channel.
PN WO9941372-A1.
PD 19-AUG-1999.
PA (ZENE) ZENECA LTD.
Query Match 6.1%; Score 73; DB 2; Length 495;
Best Local Similarity 23.2%; Pred. No. 36;
RESULT 876
ID ABO63300 standard; protein; 501 AA.
DE Klebsiella pneumoniae polypeptide seqid 9817.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73; DB 7; Length 501;
Best Local Similarity 26.5%; Pred. No. 36;
RESULT 877
ID ABP53583 standard; protein; 526 AA.
DE Human NOV13b protein SEQ ID NO:30.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 5; Length 526;
Best Local Similarity 23.3%; Pred. No. 39;
RESULT 878
ID ADH42229 standard; protein; 526 AA.
DE Novel human protein NOV50d.
PN WO2003102159-A2.
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP. 6.1%; Score 73; DB 8; Length 526;
Query Match
Best Local Similarity 23.3%; Pred. No. 39;
RESULT 879
ID ABU31136 standard; protein; 553 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 6; Length 553;
Best Local Similarity 19.6%; Pred. No. 41;
RESULT 880
ID AAG24011 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.1%; Score 73; DB 3; Length 556;
Best Local Similarity 22.0%; Pred. No. 42;
RESULT 881
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 717;
Best Local Similarity 21.3%; Pred. No. 59;
RESULT 882
ID AAW26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 2; Length 746;
Best Local Similarity 23.3%; Pred. No. 63;
RESULT 883
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 748;
Best Local Similarity 23.3%; Pred. No. 63;
RESULT 884
ID AAW88407 standard; protein; 750 AA.
DE Human adult neural tissue secreted protein s195_10.
PN WO9857976-A1.
PD 23-DEC-1998.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 2; Length 750;
Best Local Similarity 19.5%; Pred. No. 63;
RESULT 885
ID AAW26672 standard; protein; 788 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 2; Length 788;
Best Local Similarity 23.3%; Pred. No. 68;
RESULT 886
ID ABU42392 standard; protein; 788 AA.
DE Protein encoded by Prokaryotic essential gene #27919.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 6; Length 788;
Best Local Similarity 23.3%; Pred. No. 68;
RESULT 887
ID AAU36734 standard; protein; 792 AA.
DE Staphylococcus aureus cellular proliferation protein #904.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 792;

Best Local Similarity 23.3%; Pred. No. 68;
RESULT 888
ID ABU19057 standard; protein; 792 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match
Best Local Similarity 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 68;
RESULT 889
ID ABM73117 standard; protein; 792 AA.
DE Staphylococcus aureus protein #2357.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 68;
RESULT 890
ID AAW68466 standard; protein; 845 AA.
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN WO9825960-A1.
PD 18-JUN-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Query Match
Best Local Similarity 6.1%; Score 73; DB 2; Length 845;
Best Local Similarity 26.2%; Pred. No. 75;
RESULT 891
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 913;
Best Local Similarity 19.5%; Pred. No. 83;
RESULT 892
ID AAM51861 standard; protein; 966 AA.
DE Murine polycystic kidney disease protein 2.
PN WO200177331-A1.
PD 18-OCT-2001.
PA (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 893
ID ABB07819 standard; protein; 966 AA.
DE Mouse polycystic kidney disease protein 2.
PN US2002035056-A1.
PD 21-MAR-2002.
PA (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
Query Match
Best Local Similarity 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 894
ID ADJ76159 standard; protein; 966 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1411.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 8; Length 966;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 895
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 971;
Best Local Similarity 19.5%; Pred. No. 90;
RESULT 896
ID ABG07373 standard; protein; 976 AA.
DE Novel human diagnostic protein #7364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 976;

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Best Local Similarity 19.5%; Pred. No. 91;
RESULT 897
ID ABU05456 standard; protein; 209 AA.
DE M. tuberculosis and M. leprae marker protein #107.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTEUR.
Query Match 6.1%; Score 72.5; DB 5; Length 209;
Best Local Similarity 22.1%; Pred. No. 12;
RESULT 898
ID ABU15302 standard; protein; 222 AA.
DE Protein encoded by Prokaryotic essential gene #829.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITFA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 222;
Best Local Similarity 20.5%; Pred. No. 13;
RESULT 899
ID ABB53879 standard; protein; 307 AA.
DE Lactococcus lactis protein yfgg.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 307;
Best Local Similarity 22.9%; Pred. No. 21;
RESULT 900
ID ABB53675 standard; protein; 325 AA.
DE Lactococcus lactis protein ydhB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 325;
Best Local Similarity 25.9%; Pred. No. 23;
RESULT 901
ID ADH87677 standard; protein; 353 AA.
DE Enterococcus faecalis polypeptide #2157.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 353;
Best Local Similarity 21.5%; Pred. No. 25;
RESULT 902
ID ADH87557 standard; protein; 359 AA.
DE Enterococcus faecalis polypeptide #2037.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 359;
Best Local Similarity 25.0%; Pred. No. 26;
RESULT 903
ID AAR37264 standard; protein; 389 AA.
DE Oxytocin receptor.
PN EP542424-A1.
PD 19-MAY-1993.
PA (ROHT ) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 904
ID AAW23832 standard; protein; 389 AA.
DE Human oxytocin receptor.
PN EP811684-A2.
PD 10-DEC-1997.
PA (ROHT ) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 905
ID AAM40217 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 3362.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 6.1%; Score 72.5; DB 4; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 906
ID ABP81865 standard; protein; 389 AA.
DE Human oxytocin receptor protein SEQ ID NO:215.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 907
ID AAR38317 standard; protein; 389 AA.
DE Human oxytocin receptor protein.
PN WO200306402-A1.
PD 07-AUG-2003.
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 908
ID ADF12125 standard; protein; 389 AA.
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN WO2003091816-A2.
PD 13-NOV-2003.
PA (FARB ) BAYER AG.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 909
ID ADI03915 standard; protein; 389 AA.
DE Human oxytocin receptor polypeptide.
PN WO2004000993-A2.
PD 31-DEC-2003.
PA (UYQU-) UNIV QUEBEC A MONTREAL.
PA (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 910
ID ADO29590 standard; protein; 389 AA.
DE Human GPCR OXTR, SEQ ID NO:692.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 29;
RESULT 911
ID AAR58665 standard; protein; 448 AA.
DE Bovine PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 448;
Best Local Similarity 29.6%; Pred. No. 35;
RESULT 912
ID AAR58663 standard; protein; 476 AA.
DE Bovine PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 476;
Best Local Similarity 29.6%; Pred. No. 39;
RESULT 913
ID AAR58657 standard; protein; 485 AA.
DE Bovine PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 485;
Best Local Similarity 29.6%; Pred. No. 40;
RESULT 914
ID AAR58655 standard; protein; 513 AA.
DE Bovine PACAP receptor type 1A protein.
PN EP618291-A2.
PD 05-OCT-1994.
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PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 513;
Best Local Similarity 29.6%; Pred. No. 43;
RESULT 915
ID ADI1620 standard; protein; 769 AA.
DE C. elegans protein similar to Pfam PF00023.
PN US2004009537-A1.
PD 15-JAN-2004.
PA (ROOS//) ROOS J.
PA (STAU//) STAUDERMAN K.
PA (VELI//) VELICELEBI G.
Query Match 6.1%; Score 72.5; DB 8; Length 769;
Best Local Similarity 20.2%; Pred. No. 75;
RESULT 916
ID ABB05429 standard; protein; 848 AA.
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN WO200196585-A2.
PD 20-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.1%; Score 72.5; DB 5; Length 848;
Best Local Similarity 22.3%; Pred. No. 86;
RESULT 917
ID AAE31528 standard; protein; 848 AA.
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN WO200281696-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 72.5; DB 6; Length 848;
Best Local Similarity 22.3%; Pred. No. 86;
RESULT 918
ID ABU25159 standard; protein; 851 AA.
DE Protein encoded by Prokaryotic essential gene #10686.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 851;
Best Local Similarity 20.5%; Pred. No. 86;
RESULT 919
ID AAR34580 standard; protein; 3010 AA.
DE Human hepatitis C virus gene encoded polypeptide.
PN EP541089-A2.
PD 12-MAY-1993.
PA (SANW) SANWA KAGAKU KENKUSHO CO.
Query Match 6.1%; Score 72.5; DB 2; Length 3010;
Best Local Similarity 23.7%; Pred. No. 5e+02;
RESULT 920
ID ABB48543 standard; protein; 306 AA.
DE Listeria monocytogenes protein #1247.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 72; DB 5; Length 306;
Best Local Similarity 21.0%; Pred. No. 24;
RESULT 921
ID ABU3432 standard; protein; 317 AA.
DE Protein encoded by Prokaryotic essential gene #24959.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 317;
Best Local Similarity 23.5%; Pred. No. 25;
RESULT 922
ID AAB53392 standard; protein; 334 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:932.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72; DB 3; Length 334;
Best Local Similarity 28.8%; Pred. No. 27;
RESULT 923
ID AAY87505 standard; protein; 370 AA.
DE Human G coupled-protein receptor, HGR3.
PN WO200017641-A1.

PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 370;
Best Local Similarity 21.8%; Pred. No. 31;
RESULT 924
ID AAW20731 standard; protein; 375 AA.
DE H. pylori inner membrane protein, 06cpl1118orf6.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.0%; Score 72; DB 2; Length 375;
Best Local Similarity 20.9%; Pred. No. 32;
RESULT 925
ID ASU19332 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #5459.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 396;
Best Local Similarity 21.8%; Pred. No. 34;
RESULT 926
ID AEG25051 standard; protein; 414 AA.
DE Novel human diagnostic protein #25042.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72; DB 4; Length 414;
Best Local Similarity 22.6%; Pred. No. 36;
RESULT 927
ID AAG50203 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 38;
RESULT 928
ID AAG50202 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 38;
RESULT 929
ID ABM72825 standard; protein; 447 AA.
DE Staphylococcus aureus protein #2065.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 72; DB 6; Length 447;
Best Local Similarity 23.9%; Pred. No. 40;
RESULT 930
ID ABB62902 standard; protein; 448 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 448;
Best Local Similarity 25.1%; Pred. No. 41;
RESULT 931
ID ABJ18913 standard; protein; 453 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.0%; Score 72; DB 6; Length 453;
Best Local Similarity 23.9%; Pred. No. 41;
RESULT 932
ID ABU16441 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #1968.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 453;

Best Local Similarity 23.9%; Pred. No. 41;
RESULT 933
ID ADN73057 standard; protein; 468 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.0%; Score 72; DB 8; Length 468;
Best Local Similarity 21.8%; Pred. No. 43;
RESULT 934
ID AAG16338 standard; protein; 495 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 495;
Best Local Similarity 21.3%; Pred. No. 47;
RESULT 935
ID AAG16337 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 497;
Best Local Similarity 21.3%; Pred. No. 47;
RESULT 936
ID AAG16336 standard; protein; 507 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 507;
Best Local Similarity 21.3%; Pred. No. 48;
RESULT 937
ID ABU25738 standard; protein; 552 AA.
DE Protein encoded by Prokaryotic essential gene #11265.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (SLIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 552;
Best Local Similarity 19.5%; Pred. No. 54;
RESULT 938
ID AAG50201 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 556;
Best Local Similarity 22.0%; Pred. No. 55;
RESULT 939
ID ADU69383 standard; protein; 594 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 6.0%; Score 72; DB 7; Length 594;
Best Local Similarity 20.8%; Pred. No. 60;
RESULT 940
ID ABP97202 standard; protein; 696 AA.
DE Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 75;
RESULT 941
ID ABP97201 standard; protein; 696 AA.
DE Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 75;
RESULT 942
ID ABP81969 standard; protein; 696 AA.
DE Human GPCR XPR1 protein SEQ ID NO:424.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 75;
RESULT 943
ID ADB67652 standard; protein; 696 AA.
DE Human xenotropic & polytropic retrovirus receptor, SEQ ID 21.
PN WO2003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match 6.0%; Score 72; DB 7; Length 696;
Best Local Similarity 20.8%; Pred. No. 75;
RESULT 944
ID ABM69179 standard; protein; 724 AA.
DE Photorhabdus luminescens protein sequence #2276.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 72; DB 6; Length 724;
Best Local Similarity 21.3%; Pred. No. 79;
RESULT 945
ID AAB46702 standard; protein; 741 AA.
DE P. faiciparum DNA polymerase protein fragment SEQ ID NO 11.
PN WO200075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS EHF.
Query Match 6.0%; Score 72; DB 4; Length 741;
Best Local Similarity 30.4%; Pred. No. 81;
RESULT 946
ID AAM47977 standard; protein; 788 AA.
DE Human hARRG.
PN CN1315342-A.
PD 03-OCT-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.0%; Score 72; DB 5; Length 788;
Best Local Similarity 26.3%; Pred. No. 89;
RESULT 947
ID ABB58917 standard; protein; 1275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 1275;
Best Local Similarity 19.0%; Pred. No. 1.7e+02;
RESULT 948
ID AAY70064 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-1 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 3.9e+02;
RESULT 949
ID AAY70065 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-3 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 3.9e+02;
RESULT 950
ID AAY70066 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-4 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 3.9e+02;
RESULT 951
ID AAM93791 standard; protein; 208 AA.
DE Human polypeptide, SEQ ID NO: 3817.

PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 6.0%; Score 71.5; DB 4; Length 208;
 Best Local Similarity 25.2%; Pred. No. 16;
 RESULT 952
 ID ADL31784 standard; protein; 208 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 3817.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIO TECHNOLOGY.
 Query Match 6.0%; Score 71.5; DB 8; Length 208;
 Best Local Similarity 25.2%; Pred. No. 16;
 RESULT 953
 ID AAG56417 standard; protein; 209 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (REAS-) RES ASSOC BIO TECHNOLOGY.
 Query Match 6.0%; Score 71.5; DB 3; Length 209;
 Best Local Similarity 25.6%; Pred. No. 16;
 RESULT 954
 ID AAG56416 standard; protein; 216 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (REAS-) RES ASSOC BIO TECHNOLOGY.
 Query Match 6.0%; Score 71.5; DB 3; Length 216;
 Best Local Similarity 25.6%; Pred. No. 17;
 RESULT 955
 ID AAG16922 standard; protein; 218 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (REAS-) RES ASSOC BIO TECHNOLOGY.
 Query Match 6.0%; Score 71.5; DB 3; Length 218;
 Best Local Similarity 25.6%; Pred. No. 17;
 RESULT 956
 ID ABB53486 standard; protein; 301 AA.
 DE Lactococcus lactis protein ybiG.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 6.0%; Score 71.5; DB 5; Length 301;
 Best Local Similarity 26.5%; Pred. No. 27;
 RESULT 957
 ID AAW37976 standard; protein; 342 AA.
 DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
 PN WO9815289-A1.
 PD 16-APR-1998.
 PA (CORR) CORNELL RES FOUND INC.
 Query Match 6.0%; Score 71.5; DB 2; Length 342;
 Best Local Similarity 22.2%; Pred. No. 32;
 RESULT 958
 ID ADG87423 standard; protein; 348 AA.
 DE Meloidogyne incognita plki protein.
 PN US2003150017-A1.
 PD 07-AUG-2003.
 PA (MESA) MESA J R B.
 PA (GRAH) GRAHAM M W.
 PA (FAIR) FAIRBAIRN D J.
 Query Match 6.0%; Score 71.5; DB 7; Length 348;
 Best Local Similarity 21.0%; Pred. No. 33;
 RESULT 959
 ID AAR88410 standard; protein; 366 AA.
 DE High-affinity melatonin-1a receptor.
 PN WO9535320-A1.
 PD 28-DEC-1995.
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
 Query Match 6.0%; Score 71.5; DB 2; Length 366;
 Best Local Similarity 23.1%; Pred. No. 35;
 RESULT 960
 ID ASU03456 standard; protein; 382 AA.
 DE Angiogenesis-associated human protein sequence #1.
 PN WO200279492-A2.
 PD 10-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 961
 ID ABP58069 standard; protein; 382 AA.
 DE Human G-protein coupled receptor GAVE1.
 PN WO200295056-A2.
 PD 28-NOV-2002.
 PA (AVET) AVENTIS PHARM INC.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 962
 ID ABP59277 standard; protein; 382 AA.
 DE Human Edgi receptor.
 PN WO2003006503-A1.
 PD 23-JAN-2003.
 PA (CERE-) CERTEK.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 963
 ID ABU08809 standard; protein; 382 AA.
 DE Human EDG-1 protein.
 PN US2002155512-A1.
 PD 24-OCT-2002.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 964
 ID ABR59701 standard; protein; 382 AA.
 DE Human endothelial differentiation sphingolipid GPCR 1.
 PN WO2003029277-A2.
 PD 10-APR-2003.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 965
 ID ABP81876 standard; protein; 382 AA.
 DE Human sphingolipid receptor Edgi protein SEQ ID NO:237.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 Query Match 6.0%; Score 71.5; DB 6; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 966
 ID ADB67662 standard; protein; 382 AA.
 DE Human EDG1, SEQ ID 31.
 PN WO2003072824-A1.
 PD 04-SEP-2003.
 PA (SANY) SANKYO CO LTD.
 Query Match 6.0%; Score 71.5; DB 7; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 967
 ID ADC40477 standard; protein; 382 AA.
 DE Protein of human EDG-1.
 PN WO2003052096-A1.
 PD 26-JUN-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 6.0%; Score 71.5; DB 7; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 968
 ID ADN38684 standard; protein; 382 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 6.0%; Score 71.5; DB 7; Length 382;
 Best Local Similarity 22.3%; Pred. No. 37;
 RESULT 969
 ID ADJ45541 standard; protein; 382 AA.
 DE LXR-ligand induced transcript seq id 72.
 PN US2004023276-A1.
 PD 05-FEB-2004.
 PA (WARD) WARD T R.

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PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.
Query Match 6.0%; Score 71.5; DB 8; Length 382;
Best Local Similarity 22.3%; Pred. No. 37;
RESULT 970
ID ABB05226 standard; protein; 390 AA.
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN WO200192296-A2.
PD 08-DEC-2001.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 5; Length 390;
Best Local Similarity 22.2%; Pred. No. 38;
RESULT 971
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 6.0%; Score 71.5; DB 7; Length 394;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 972
ID ABB48023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 71.5; DB 5; Length 435;
Best Local Similarity 21.4%; Pred. No. 45;
RESULT 973
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.0%; Score 71.5; DB 2; Length 441;
Best Local Similarity 22.6%; Pred. No. 45;
RESULT 974
ID ABP75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 6; Length 470;
Best Local Similarity 22.4%; Pred. No. 50;
RESULT 975
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 524;
Best Local Similarity 26.6%; Pred. No. 58;
RESULT 976
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.
PN WO200300012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 565;
Best Local Similarity 22.4%; Pred. No. 64;
RESULT 977
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN WO9821242-A1.
PD 22-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 71.5; DB 2; Length 568;
Best Local Similarity 22.4%; Pred. No. 65;
RESULT 978
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 70;
RESULT 979
ID ABM72619 standard; protein; 603 AA.
DE Staphylococcus aureus protein #1859.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 70;
RESULT 980
ID ADM43215 standard; protein; 697 AA.
DE Human methionine synthase reductase del Arg 559 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 981
ID ADM43217 standard; protein; 697 AA.
DE Human methionine synthase reductase del Leu 576 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 982
ID AAB07591 standard; protein; 698 AA.
DE A human methionine synthase reductase polypeptide.
PN WO200042196-A2.
PD 20-JUL-2000.
PA (UYMC-) UNIV MCGILL.
Query Match 6.0%; Score 71.5; DB 3; Length 698;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 983
ID AEG00883 standard; protein; 698 AA.
DE Novel human diagnostic protein #874.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HVSE-) HVSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 698;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 984
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met221le variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 985
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys377Tyr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.

PA (ROSE/) ROSENBLATT D. 6.0%; Score 71.5; DB 7; Length 698;
Query Match 22.8%; Pred. No. 86;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 986
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D. 6.0%; Score 71.5; DB 7; Length 698;
Query Match 22.8%; Pred. No. 86;
Best Local Similarity 22.8%; Pred. No. 86;
RESULT 987
ID AAY51606 standard; protein; 890 AA.
DE Human wmi protein.
PN DE19845277-Cl.
PD 09-MAR-2000.
PA (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
Query Match 6.0%; Score 71.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.2e+02;
RESULT 988
ID ABB78282 standard; protein; 890 AA.
DE Amino acid sequence of human wolframin polypeptide.
PN WO200263307-A2.
PD 15-AUG-2002.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.0%; Score 71.5; DB 5; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.2e+02;
RESULT 989
ID ADD46013 standard; protein; 890 AA.
DE Human Protein O76024, SEQ ID NO 11685.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.2e+02;
RESULT 990
ID ADF69127 standard; protein; 890 AA.
DE Human MF53 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.2e+02;
RESULT 991
ID ADL22689 standard; protein; 2245 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 7; Length 2245;
Best Local Similarity 22.4%; Pred. No. 4.3e+02;
RESULT 992
ID AAB42192 standard; protein; 2405 AA.
DE Human OREF ORF1956 polypeptide sequence SEQ ID NO:3912.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 71.5; DB 3; Length 2405;
Best Local Similarity 22.4%; Pred. No. 4.8e+02;
RESULT 993
ID ABB11404 standard; peptide; 2560 AA.
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN WO200157118-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 2560;
Best Local Similarity 22.4%; Pred. No. 5.2e+02;
RESULT 994

ID ABU11556 standard; protein; 2894 AA.
DE Human MDDT polypeptide SEQ ID 503.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 6; Length 2894;
Best Local Similarity 22.4%; Pred. No. 6.2e+02;
RESULT 995
ID AAU07054 standard; protein; 2923 AA.
DE Human Flamingo protein encoded by cDNA splice variant.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.0%; Score 71.5; DB 4; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 996
ID AAM50866 standard; protein; 2923 AA.
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN WO200208765-A2.
PD 31-JAN-2002.
PA (GENO-) APPLIED GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 5; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 997
ID ABP82018 standard; protein; 2923 AA.
DE Human GPCR CELSR2 protein SEQ ID NO:524.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.0%; Score 71.5; DB 6; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 998
ID ADC15499 standard; protein; 2923 AA.
DE Human cadherin EGF LAG seven-pass G-type receptor 2.
PN US2003086934-A1.
PD 08-MAY-2003.
PA (BOTS/) BOTSTEIN D.
PA (BROW/) BROWN P O.
PA (PERO/) PEROU C M.
PA (RING/) RING B.
PA (ROSS/) ROSS D.
PA (SEIT/) SEITZ R.
PA (VRIJ/) VAN DE RIJN J M.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 999
ID ADC86479 standard; protein; 2923 AA.
DE Human GPCR protein SEQ ID NO:932.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 1000
ID ADE54407 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 210.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 1001
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;

RESULT 1002
ID ADO29245 standard; protein; 2923 AA.
DE Human GPCR CELSR2, SEQ ID NO:346.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.0%; Score 71.5; DB 8; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 1003
ID AAU74826 standard; protein; 2936 AA.
DE Human REPT9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 5; Length 2936;
Best Local Similarity 22.4%; Pred. No. 6.3e+02;
RESULT 1004
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.0%; Score 71.5; DB 4; Length 2956;
Best Local Similarity 22.4%; Pred. No. 6.4e+02;
RESULT 1005
ID AR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JKL-B.
PN JPO5068562-A.
PD 23-MAR-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 23.7%; Pred. No. 6.5e+02;
RESULT 1006
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polypeptide.
PN WO9300365-A2.
PD 07-JAN-1993.
PA (CHIR) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 22.8%; Pred. No. 6.5e+02;
RESULT 1007
ID ABB67866 standard; protein; 5303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 71.5; DB 4; Length 5303;
Best Local Similarity 29.5%; Pred. No. 1.4e+03;
RESULT 1008
ID ABB06793 standard; protein; 198 AA.
DE Human transmembrane 4 protein 22 SEQ ID NO:2.
PN CNJ327990-A.
PD 26-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 5.9%; Score 71; DB 5; Length 198;
Best Local Similarity 24.5%; Pred. No. 17;
RESULT 1009
ID ABR58388 standard; protein; 240 AA.
DE Human NOV17a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 240;
Best Local Similarity 18.6%; Pred. No. 22;
RESULT 1010
ID ABP26255 standard; protein; 295 AA.
DE Streptococcus polypeptide SEQ ID NO 1686.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 71; DB 5; Length 295;
Best Local Similarity 24.9%; Pred. No. 30;

RESULT 1011
ID AAG72952 standard; protein; 310 AA.
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
Query Match 5.9%; Score 71; DB 4; Length 310;
Best Local Similarity 22.9%; Pred. No. 32;
RESULT 1012
ID AAR48717 standard; protein; 312 AA.
DE G-protein coupled human interleukin-8 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UVNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 32;
RESULT 1013
ID AAW02689 standard; peptide; 312 AA.
DE G-protein coupled human interleukin-8 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UVNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 32;
RESULT 1014
ID AAG72169 standard; protein; 312 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 32;
RESULT 1015
ID AAG72377 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 32;
RESULT 1016
ID ABB54394 standard; protein; 391 AA.
DE Lactococcus lactis protein YK11.
PN FR2807445-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.9%; Score 71; DB 5; Length 391;
Best Local Similarity 20.3%; Pred. No. 44;
RESULT 1017
ID ABB48413 standard; protein; 423 AA.
DE Listeria monocytogenes protein #1117.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.9%; Score 71; DB 5; Length 423;
Best Local Similarity 28.4%; Pred. No. 49;
RESULT 1018
ID ADL05302 standard; protein; 423 AA.
DE M. catarrhalis protein #1068.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 71; DB 8; Length 423;
Best Local Similarity 38.0%; Pred. No. 49;
RESULT 1019
ID ADJ95142 standard; protein; 444 AA.
DE Novel NOVA protein sequence #185.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.

Query Match 5.9%; Score 71; DB 7; Length 444;
 Best Local Similarity 21.0%; Pred. No. 52;
 RESULT 1020
 ID ADJ95144 standard; protein; 444 AA.
 DE Novel NOVX protein sequence #186.
 PN WO2003040325-A2.
 PD 15-MAY-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 71; DB 7; Length 444;
 Best Local Similarity 21.0%; Pred. No. 52;
 RESULT 1021
 ID ADP29417 standard; protein; 455 AA.
 DE Human secreted protein SEQ ID #184.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 5.9%; Score 71; DB 8; Length 455;
 Best Local Similarity 24.3%; Pred. No. 54;
 RESULT 1022
 ID ABU19912 standard; protein; 457 AA.
 DE Protein encoded by Prokaryotic essential gene #5439.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 71; DB 6; Length 457;
 Best Local Similarity 22.0%; Pred. No. 55;
 RESULT 1023
 ID ADI24575 standard; protein; 470 AA.
 DE Human endogenous 5HT2A serotonin receptor.
 PN US2003224442-A1.
 PD 04-DEC-2003.
 PA (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 PA (LIAW/) LIAW C W.
 PA (RUSS/) RUSSO J F.
 PA (THOM/) THOMSEN W J.
 Query Match 5.9%; Score 71; DB 8; Length 470;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1024
 ID AAR37659 standard; protein; 471 AA.
 DE Sequence encoded by cDNA.
 PN WO9311257-A2.
 PD 10-JUN-1993.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1025
 ID AAW23781 standard; protein; 471 AA.
 DE Human serotonin 5-HT2 receptor protein.
 PN US5661024-A.
 PD 26-AUG-1997.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1026
 ID AAW77107 standard; protein; 471 AA.
 DE Human 5-HT2A serotonin receptor.
 PN WO938217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1027
 ID AAY90640 standard; protein; 471 AA.
 DE Human G protein-coupled receptor 5HT-2A (serotonin receptor).
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match 5.9%; Score 71; DB 3; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1028

ID AAY90675 standard; protein; 471 AA.
 DE Human mutant G protein-coupled receptor 5HT-2A.
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match 5.9%; Score 71; DB 3; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1029
 ID ABB07978 standard; protein; 471 AA.
 DE Human 5-HT2 receptor sequence.
 PN US6383762-B1.
 PD 07-MAY-2002.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match 5.9%; Score 71; DB 5; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1030
 ID ABP81765 standard; protein; 471 AA.
 DE Human 5-HT2A receptor protein SEQ ID NO:12.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 Query Match 5.9%; Score 71; DB 6; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1031
 ID ADC22641 standard; protein; 471 AA.
 DE Human G protein-coupled receptor (GPCR) polypeptide #32.
 PN US6555339-B1.
 PD 29-APR-2003.
 PA (AREN-) ARENA PHARM INC.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1032
 ID ADC22747 standard; protein; 471 AA.
 DE Human G protein-coupled receptor (GPCR) polypeptide #72.
 PN US6555339-B1.
 PD 29-APR-2003.
 PA (AREN-) ARENA PHARM INC.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1033
 ID ADE65844 standard; protein; 471 AA.
 DE Human serotonin 2A receptor.
 PN US2003170723-A1.
 PD 11-SEP-2003.
 PA (SATO/) SATO T.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1034
 ID ADH14220 standard; protein; 471 AA.
 DE Mutated human serotonin 5HT_2A.
 PN US2003105292-A1.
 PD 05-JUN-2003.
 PA (LIAW/) LIAW C W.
 PA (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1035
 ID ADH14114 standard; protein; 471 AA.
 DE Human serotonin 5HT_2A.
 PN US2003105292-A1.
 PD 05-JUN-2003.
 PA (LIAW/) LIAW C W.
 PA (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 57;
 RESULT 1036
 ID ADL90125 standard; protein; 471 AA.
 DE Human serotonin receptor 5HT2a.
 PN US2003167476-A1.
 PD 04-SEP-2003.
 PA (CONK/) CONKLIN B R.

Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 57;
RESULT 1037
ID ADO29506 standard; protein; 471 AA.
DE Human GPCR HTR2A, SEQ ID NO:608.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIN-) PRIMAL INC.
Query Match 5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 57;
RESULT 1038
ID RAY01626 standard; protein; 478 AA.
DE Amino acid sequence of the human 5-HT2 receptor.
PN US5885785-A.
PD 23-MAR-1999.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 71; DB 2; Length 478;
Best Local Similarity 23.7%; Pred. No. 58;
RESULT 1039
ID ABG70577 standard; protein; 480 AA.
DE Human serotonin (5-HT2) receptor.
PN US2002098548-A1.
PD 25-JUL-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 71; DB 5; Length 480;
Best Local Similarity 23.7%; Pred. No. 58;
RESULT 1040
ID ABM70440 standard; protein; 493 AA.
DE Photorehabdus luminescens protein sequence #3537.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 5.9%; Score 71; DB 6; Length 493;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 1041
ID ADE56383 standard; protein; 545 AA.
DE Rat Protein O70536, SEQ ID NO 2235.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 70;
RESULT 1042
ID ADD48660 standard; protein; 545 AA.
DE Rat Protein BAA25372, SEQ ID NO 14366.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 70;
RESULT 1043
ID ABJ26399 standard; protein; 559 AA.
DE Aspergillus fumigatus essential gene protein #1057.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 559;
Best Local Similarity 23.1%; Pred. No. 72;
RESULT 1044
ID ABP35686 standard; protein; 563 AA.
DE Fungal ZBC protein sequence #112.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 5.9%; Score 71; DB 5; Length 563;
Best Local Similarity 19.1%; Pred. No. 73;
RESULT 1045
ID AAB20578 standard; protein; 564 AA.
DE Mouse OCTN3 protein SEQ ID NO:1.
PN WO200046368-A1.

PD 10-AUG-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.9%; Score 71; DB 3; Length 564;
Best Local Similarity 21.4%; Pred. No. 73;
RESULT 1046
ID ABB91532 standard; protein; 676 AA.
DE Herbicidally active polypeptide SEQ ID NO 743.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 5; Length 676;
Best Local Similarity 22.3%; Pred. No. 94;
RESULT 1047
ID AAE21800 standard; protein; 727 AA.
DE Human HIPHUM 0000029 protein.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.9%; Score 71; DB 5; Length 727;
Best Local Similarity 24.3%; Pred. No. 1e+02;
RESULT 1048
ID ABU54636 standard; protein; 727 AA.
DE Human NOVX polypeptide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 727;
Best Local Similarity 24.3%; Pred. No. 1e+02;
RESULT 1049
ID ADH76500 standard; protein; 727 AA.
DE 727 amino acid human neurotransmitter transporter protein.
PN US2003219774-A1.
PD 27-NOV-2003.
PA (SHAR) SHARMA R.
PA (RAMA) RAMANATHAN C S.
PA (WEST) WESTPHAL R.
PA (FEDE) FEDER J N.
PA (LEEL) LEE L M.
Query Match 5.9%; Score 71; DB 8; Length 727;
Best Local Similarity 24.3%; Pred. No. 1e+02;
RESULT 1050
ID ABR62929 standard; protein; 744 AA.
DE Human neurotransmitter transporter.
PN WO2003059947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 744;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1051
ID ABB60052 standard; protein; 792 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 71; DB 4; Length 792;
Best Local Similarity 17.7%; Pred. No. 1.2e+02;
RESULT 1052
ID AAR30616 standard; protein; 3010 AA.
DE Polypeptide coded by Korean HCV full cDNA sequence LBC1.
PN EP521318-A2.
PD 07-JAN-1993.
PA (LUCK-) LUCKY LTD.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 7.5e+02;
RESULT 1053
ID AAR53417 standard; protein; 3010 AA.
DE Blood transmissible NANBHV protein.
PN JP06105690-A.
PD 19-APR-1994.
PA (KAEN) KAENNO K.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 7.5e+02;
RESULT 1054

ID ABR83573 standard; protein; 202 AA.
 DE BcrC amino acid sequence SEQ ID NO:40.
 PN WO2003057708-A2.
 PD 17-JUL-2003.
 PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
 Query Match 5.9%; Score 70.5; DB 6; Length 202;
 Best Local Similarity 26.5%; Pred. No. 20;
 RESULT 1055
 ID AAU01287 standard; protein; 218 AA.
 DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.
 PN WO200125453-A2.
 PD 12-APR-2001.
 PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 Query Match 5.9%; Score 70.5; DB 4; Length 218;
 Best Local Similarity 29.3%; Pred. No. 22;
 RESULT 1056
 ID AAU97208 standard; protein; 228 AA.
 DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
 PN US6383776-B1.
 PD 07-MAY-2002.
 PA (DUPO) DU PONT DE NEMOURS & CO B I.
 Query Match 5.9%; Score 70.5; DB 5; Length 228;
 Best Local Similarity 21.6%; Pred. No. 24;
 RESULT 1057
 ID ABU0333 standard; protein; 228 AA.
 DE Wheat sugar transport protein #3.
 PN US2002178468-A1.
 PD 28-NOV-2002.
 PA (ALLE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match 5.9%; Score 70.5; DB 6; Length 228;
 Best Local Similarity 21.6%; Pred. No. 24;
 RESULT 1058
 ID ADG47920 standard; protein; 228 AA.
 DE Wheat Arabidopsis-like sugar transport protein #3.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTJARIIS T G.
 Query Match 5.9%; Score 70.5; DB 8; Length 228;
 Best Local Similarity 21.6%; Pred. No. 24;
 RESULT 1059
 ID ABU17430 standard; protein; 275 AA.
 DE Protein encoded by Prokaryotic essential gene #2957.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 6; Length 275;
 Best Local Similarity 22.8%; Pred. No. 31;
 RESULT 1060
 ID ABB5033 standard; protein; 285 AA.
 DE Lactococcus lactis protein malG.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 5.9%; Score 70.5; DB 5; Length 285;
 Best Local Similarity 26.1%; Pred. No. 32;
 RESULT 1061
 ID ABB05467 standard; protein; 291 AA.
 DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
 PN JP2001321171-A.
 PD 20-NOV-2001.
 PA (WARI/) WARIISHI H.
 PA (KUBI) KUBOTA CORP.
 Query Match 5.9%; Score 70.5; DB 5; Length 291;
 Best Local Similarity 29.4%; Pred. No. 33;
 RESULT 1062
 ID ADA35787 standard; protein; 297 AA.
 DE Acinetobacter baumannii protein #2948.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.9%; Score 70.5; DB 6; Length 297;
 Best Local Similarity 24.1%; Pred. No. 34;
 RESULT 1063
 ID AEM70358 standard; protein; 321 AA.
 DE Photorhabdus luminescens protein sequence #3455.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 5.9%; Score 70.5; DB 6; Length 321;
 Best Local Similarity 19.2%; Pred. No. 38;
 RESULT 1064
 ID ADH22355 standard; protein; 330 AA.
 DE Human receptor & membrane associated protein (REMAP) SeqIDS.
 PN WO2003104395-A2.
 PD 18-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 330;
 Best Local Similarity 24.2%; Pred. No. 40;
 RESULT 1065
 ID ADK68232 standard; protein; 343 AA.
 DE Novel NOVX protein #79.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 343;
 Best Local Similarity 30.0%; Pred. No. 42;
 RESULT 1066
 ID ADH72226 standard; protein; 343 AA.
 DE Human protein of the invention NOV55a SEQ ID NO:1122.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 343;
 Best Local Similarity 30.0%; Pred. No. 42;
 RESULT 1067
 ID AAR69518 standard; protein; 365 AA.
 DE Prostaglandin-EP3-9 receptor.
 PN WO9500552-A1.
 PD 05-JAN-1995.
 PA (MERI) MERCK FROSST CANADA INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 365;
 Best Local Similarity 24.2%; Pred. No. 46;
 RESULT 1068
 ID AAE38521 standard; protein; 365 AA.
 DE Human PTGER3 protein isoform, EP3b.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 365;
 Best Local Similarity 24.2%; Pred. No. 46;
 RESULT 1069
 ID ADI35077 standard; protein; 365 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 46;
 RESULT 1070
 ID ADL15889 standard; protein; 365 AA.
 DE Human prostaglandin EP3 receptor #3.
 PN US6670134-B1.
 PD 30-DEC-2003.
 PA (ALLR) ALLERGAN INC.
 PA (UYAR-) UNIV ARIZONA.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 46;
 RESULT 1071
 ID ADF04358 standard; protein; 367 AA.
 DE Bacterial polypeptide #471.
 PN US6605709-B1.
 PD 12-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 367;
Best Local Similarity 33.3%; Pred. No. 46;
RESULT 1072
ID AAE38520 standard; protein; 374 AA.
DE Human PTGER3 protein isoform, EP3d.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 374;
Best Local Similarity 24.2%; Pred. No. 47;
RESULT 1073
ID ADI35075 standard; protein; 374 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 374;
Best Local Similarity 24.2%; Pred. No. 47;
RESULT 1074
ID AAR48711 standard; protein; 379 AA.
DE G-protein coupled rat serotonin 2 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UNYU) UNIV NEW YORK STATE.
Query Match 5.9%; Score 70.5; DB 2; Length 379;
Best Local Similarity 22.9%; Pred. No. 48;
RESULT 1075
ID AAW02683 standard; peptide; 379 AA.
DE G-protein coupled rat serotonin 2 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UNYU) UNIV NEW YORK STATE.
Query Match 5.9%; Score 70.5; DB 2; Length 379;
Best Local Similarity 22.9%; Pred. No. 48;
RESULT 1076
ID AAR69517 standard; protein; 388 AA.
DE Prostaglandin-EP3-21 receptor.
PN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 388;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1077
ID AAE38513 standard; protein; 388 AA.
DE Human PTGER3 protein isoform, EP3c.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 388;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1078
ID ADI35061 standard; protein; 388 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1079
ID ADL15887 standard; protein; 388 AA.
DE Human prostaglandin EP3 receptor #2.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1080
ID AAR69516 standard; protein; 390 AA.
DE Prostaglandin-EP3-alpha receptor.
PN WO9500552-A1.
PD 05-JAN-1995.

PA (MERI) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1081
ID AAE38516 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a1.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1082
ID AAE38517 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a2.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1083
ID ADI35067 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1084
ID ADI35069 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1085
ID ADL15898 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #4.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1086
ID ADL15885 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #1.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 50;
RESULT 1087
ID AAW57411 standard; protein; 393 AA.
DE Human prostaglandin EP3-VI receptor.
PN JPI0113185-A.
PD 06-MAY-1998.
PA (ONOO) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 393;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 1088
ID AAE38519 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3e.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 1089
ID AAE38523 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3-VI.
PN WO2003064471-A2.

PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 1090
ID ADI35063 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 1091
ID ADI35073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 1092
ID AAE57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOX) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1093
ID AP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1094
ID AAE38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1095
ID ADI35079 standard; protein; 402 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1096
ID ADO5167 standard; protein; 402 AA.
DE Protein #69 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1097
ID ADO29620 standard; protein; 402 AA.
DE Human GPCR PTGER3, SEQ ID NO:722.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1098
ID AAE38514 standard; protein; 407 AA.
DE Human PTGER3 protein isoform, EP3g.
PN WO2003064471-A2.
PD 07-AUG-2003.

PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 407;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1099
ID ADI35063 standard; protein; 407 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 407;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1100
ID AAE38518 standard; protein; 425 AA.
DE Human PTGER3 protein isoform, EP3f.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 425;
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1101
ID ADI35071 standard; protein; 425 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 425;
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1102
ID AAE38515 standard; protein; 433 AA.
DE Human PTGER3 protein isoform, EP3h.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 433;
Best Local Similarity 24.2%; Pred. No. 58;
RESULT 1103
ID ADI35065 standard; protein; 433 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 433;
Best Local Similarity 24.2%; Pred. No. 58;
RESULT 1104
ID AAW98431 standard; protein; 480 AA.
DE H. pylori GPO 446 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 70.5; DB 2; Length 480;
Best Local Similarity 23.1%; Pred. No. 67;
RESULT 1105
ID ABP40525 standard; protein; 499 AA.
DE Scaphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 5; Length 499;
Best Local Similarity 20.5%; Pred. No. 71;
RESULT 1106
ID ABU30473 standard; protein; 521 AA.
DE Protein encoded by Prokaryotic essential gene #16000.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 6; Length 521;
Best Local Similarity 23.7%; Pred. No. 75;
RESULT 1107
ID AAU97213 standard; protein; 539 AA.
DE Wheat sugar transport protein encoded by wlk8.pk0001.all.
PN US6383776-B1.
PD 07-MAY-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 5.9%; Score 70.5; DB 5; Length 539;
 Best Local Similarity 26.0%; Pred. No. 79;
 RESULT 1108
 ID ABO08338 standard; protein; 539 AA.
 DE Wheat sugar transport protein #4.
 PN US2002178468-A1.
 PD 28-NOV-2002.
 PA (ALTE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match 5.9%; Score 70.5; DB 6; Length 539;
 Best Local Similarity 26.0%; Pred. No. 79;
 RESULT 1109
 ID ADG47930 standard; protein; 539 AA.
 DE Wheat Beta-vulgaris-like sugar transport protein #1.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTJARIIS T G.
 Query Match 5.9%; Score 70.5; DB 8; Length 539;
 Best Local Similarity 26.0%; Pred. No. 79;
 RESULT 1110
 ID ABO27418 standard; protein; 548 AA.
 DE Protein encoded by Prokaryotic essential gene #12945.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 6; Length 548;
 Best Local Similarity 24.0%; Pred. No. 80;
 RESULT 1111
 ID ADD46023 standard; protein; 599 AA.
 DE Rat Protein P23978, SEQ ID NO 11695.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 70.5; DB 7; Length 599;
 Best Local Similarity 20.1%; Pred. No. 91;
 RESULT 1112
 ID ABO2687 standard; protein; 599 AA.
 DE Rattus norvegicus neuronal GABA transporter (GAT-1).
 PN US2003143729-A1.
 PD 31-JUL-2003.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 599;
 Best Local Similarity 20.1%; Pred. No. 91;
 RESULT 1113
 ID AAM78767 standard; protein; 600 AA.
 DE Human protein SRQ ID NO 1429.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 70.5; DB 4; Length 600;
 Best Local Similarity 19.5%; Pred. No. 91;
 RESULT 1114
 ID ADJ64315 standard; protein; 662 AA.
 DE Cartilage differentiation inhibiting protein, SEQ ID 10.
 PN WO2004013326-A1.
 PD 12-FEB-2004.
 PA (ASAH) ASAHI KASEI KK.
 Query Match 5.9%; Score 70.5; DB 8; Length 662;
 Best Local Similarity 22.7%; Pred. No. 1e+02;
 RESULT 1115
 ID ABB92892 standard; protein; 700 AA.
 DE Herbicidally active polypeptide SEQ ID NO 2103.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 70.5; DB 5; Length 700;
 Best Local Similarity 25.8%; Pred. No. 1.1e+02;
 RESULT 1116
 ID AAB56721 standard; protein; 717 AA.

DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.
 PN WO200055174-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 Query Match 5.9%; Score 70.5; DB 3; Length 717;
 Best Local Similarity 22.4%; Pred. No. 1.2e+02;
 RESULT 1117
 ID ADG47941 standard; protein; 740 AA.
 DE Arabidopsis thaliana-like sugar transport protein #2.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTJARIIS T G.
 Query Match 5.9%; Score 70.5; DB 8; Length 740;
 Best Local Similarity 22.8%; Pred. No. 1.2e+02;
 RESULT 1118
 ID AAG39555 standard; protein; 766 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.9%; Score 70.5; DB 3; Length 766;
 Best Local Similarity 21.3%; Pred. No. 1.3e+02;
 RESULT 1119
 ID AAG39554 standard; protein; 815 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.9%; Score 70.5; DB 3; Length 815;
 Best Local Similarity 21.3%; Pred. No. 1.4e+02;
 RESULT 1120
 ID AAG39553 standard; protein; 927 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.9%; Score 70.5; DB 3; Length 927;
 Best Local Similarity 21.3%; Pred. No. 1.7e+02;
 RESULT 1121
 ID ABP73754 standard; protein; 1026 AA.
 DE Candida albicans essential protein SEQ ID NO 7591.
 PN WO200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 5; Length 1026;
 Best Local Similarity 22.3%; Pred. No. 1.9e+02;
 RESULT 1122
 ID AAW17057 standard; protein; 1027 AA.
 DE Candida albicans chitin synthase (CHS1).
 PN WO9716540-A1.
 PD 09-MAY-1997.
 PA (CHEM-) CHEMGENICS PHARM INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 1027;
 Best Local Similarity 22.3%; Pred. No. 1.9e+02;
 RESULT 1123
 ID ADH22510 standard; protein; 1147 AA.
 DE Human transporter & ion channel (TRICH) protein SeqID8.
 PN WO2003093444-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 1147;
 Best Local Similarity 19.5%; Pred. No. 2.2e+02;
 RESULT 1124
 ID ADK18350 standard; protein; 1163 AA.
 DE Human NOVX protein #2.
 PN WO2003057854-A2.
 PD 17-JUL-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 1163;
 Best Local Similarity 19.5%; Pred. No. 2.3e+02;
 RESULT 1125
 ID ADM29274 standard; protein; 1163 AA.
 DE Human novel protein NOV2b.
 PN WO2003064628-A2.
 PD 07-AUG-2003.

PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 1163;
Best Local Similarity 19.5%; Pred. No. 2.3e+02;
RESULT 1126
ID AAW53863 standard; peptide; 1780 AA.
DE Human gravin polypeptide.
PN US5741890-A.
PD 21-APR-1998.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 2; Length 1780;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1127
ID AAB15380 standard; protein; 1780 AA.
DE Human gravin protein sequence.
PN US6090929-A.
PD 18-JUL-2000.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 3; Length 1780;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1128
ID AAO17365 standard; protein; 1781 AA.
DE Human gravin.
PN EP1191107-A2.
PD 27-MAR-2002.
PA (SCHD-) SCHERING AG.
Query Match 5.9%; Score 70.5; DB 5; Length 1781;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1129
ID ABU03477 standard; protein; 1781 AA.
DE Angiogenesis-associated human protein sequence #22.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 70.5; DB 6; Length 1781;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1130
ID ABB97448 standard; protein; 1783 AA.
DE Novel human protein SEQ ID NO: 716.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 5; Length 1783;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
RESULT 1131
ID ABB21018 standard; protein; 1795 AA.
DE Novel human diagnostic protein #21009.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 4; Length 1795;
Best Local Similarity 34.8%; Pred. No. 4.2e+02;
RESULT 1132
ID AAG34242 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 185;
Best Local Similarity 26.2%; Pred. No. 20;
RESULT 1133
ID AAG34241 standard; protein; 189 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 189;
Best Local Similarity 26.2%; Pred. No. 21;
RESULT 1134
ID AAW44944 standard; protein; 225 AA.
DE Avian infectious bronchitis virus glycoprotein M.
PN FR2751225-A1.
PD 23-JAN-1998.
PA (INMR-) RHONE MERIEUX SA.
Query Match 5.9%; Score 70; DB 2; Length 225;
Best Local Similarity 21.6%; Pred. No. 27;

RESULT 1135
ID ADB09893 standard; protein; 226 AA.
DE Allostercoccus oclitis antigenic protein SEQ ID NO: 3730.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP-) WYETH HOLDINGS CORP.
Query Match 5.9%; Score 70; DB 6; Length 226;
Best Local Similarity 24.1%; Pred. No. 27;
RESULT 1136
ID AAG34240 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 235;
Best Local Similarity 26.2%; Pred. No. 28;
RESULT 1137
ID ABB69790 standard; protein; 256 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 5.9%; Score 70; DB 4; Length 256;
Best Local Similarity 20.2%; Pred. No. 32;
RESULT 1138
ID AAG53762 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 274;
Best Local Similarity 26.0%; Pred. No. 35;
RESULT 1139
ID AAG53761 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 287;
Best Local Similarity 26.0%; Pred. No. 38;
RESULT 1140
ID AEU35677 standard; protein; 292 AA.
DE Protein encoded by Prokaryotic essential gene #21204.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 292;
Best Local Similarity 22.5%; Pred. No. 38;
RESULT 1141
ID ADK48488 standard; protein; 307 AA.
DE Streptococcus pneumoniae protein, Seq ID No 5003.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 307;
Best Local Similarity 26.2%; Pred. No. 41;
RESULT 1142
ID AAR72985 standard; protein; 333 AA.
DE Epsilon opioid receptor.
PN WO9512670-A1.
PD 11-MAY-1995.
PA (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
Query Match 5.9%; Score 70; DB 2; Length 333;
Best Local Similarity 23.8%; Pred. No. 46;
RESULT 1143
ID AAY90613 standard; protein; 333 AA.
DE Human G protein-coupled receptor GPR8.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 3; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1144
ID AAY90647 standard; protein; 333 AA.
DE Human mutant G protein-coupled receptor GPR8 (T259K).
PN WO200022129-A1.

PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 3; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1145
ID AAU01297 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8, mutant N127A.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1146
ID AAU01295 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1147
ID AAU01298 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8, mutant T259E.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1148
ID ABB84683 standard; protein; 333 AA.
DE Human GPR8-ligand related protein #1.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1149
ID ABB84723 standard; protein; 333 AA.
DE Human GPR8-ligand related protein #3.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1150
ID ABG65918 standard; protein; 333 AA.
DE G protein-coupled receptor related peptide #6.
PN WO200243368-A1.
PD 06-JUN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1151
ID ABU61448 standard; protein; 333 AA.
DE Screening method related protein #1.
PN WO200293161-A1.
PD 21-NOV-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1152
ID AB37874 standard; protein; 333 AA.
DE GPR7 ligand related human protein SEQ ID No 84.
PN WO2002102847-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1153
ID ABP81897 standard; protein; 333 AA.
DE Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1154
ID ABR57245 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:84.
PN WO2003045994-A1.
PD 05-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1155
ID ADC22691 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #44.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1156
ID ADC22535 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #5.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1157
ID ADC51793 standard; protein; 333 AA.
DE Human GPR8, SEQ ID 4.
PN WO2003057236-A1.
PD 17-JUL-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1158
ID ABR61545 standard; protein; 333 AA.
DE Human GPR8 receptor polypeptide.
PN WO2003081234-A2.
PD 02-OCT-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1159
ID ADG41976 standard; protein; 333 AA.
DE Human GPR8 polypeptide.
PN JP2003009867-A.
PD 14-JAN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1160
ID ADH14008 standard; protein; 333 AA.
DE Human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1161
ID ADH14164 standard; protein; 333 AA.
DE Mutated human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;

Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1162
ID ADG12852 standard; protein; 333 AA.
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1163
ID ADO29700 standard; protein; 333 AA.
DE Human GPCR GPR8, SEQ ID NO:802.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1164
ID ADO31044 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:73.
PN WO2004041301-A1.
PD 21-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1165
ID ADO19919 standard; protein; 333 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 46;
RESULT 1166
ID ADG12854 standard; protein; 347 AA.
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 347;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1167
ID ABG30839 standard; protein; 364 AA.
DE Human calcium channel protein.
PN WO200252003-A2.
PD 04-JUL-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 5; Length 364;
Best Local Similarity 25.0%; Pred. No. 52;
RESULT 1168
ID ADG12856 standard; protein; 364 AA.
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 52;
RESULT 1169
ID ADO28778 standard; protein; 364 AA.
DE Human GPR8-enhanced receptor.
PN WO2004091946-A1.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 52;
RESULT 1170
ID ADG12858 standard; protein; 378 AA.
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
PN WO2003097795-A2.
PD 27-NOV-2003.

PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 378;
Best Local Similarity 23.8%; Pred. No. 55;
RESULT 1171
ID ADN49121 standard; protein; 388 AA.
DE Mouse oxytocin receptor protein.
PN US2004086881-A1.
PD 06-MAY-2004.
PA (RAMA/) RAMANATHAN C S.
PA (GOPA/) GOPAL S.
PA (MINT/) MINTIER G A.
PA (FEDE/) FEDER J.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 57;
RESULT 1172
ID ADO29591 standard; protein; 388 AA.
DE Mouse GPCR OXTR, SEQ ID NO:693.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 57;
RESULT 1173
ID ADA54410 standard; protein; 399 AA.
DE Human protein, SEQ ID 1978.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 59;
RESULT 1174
ID AEG99947 standard; protein; 399 AA.
DE Human novel polypeptide #60.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 59;
RESULT 1175
ID ADC96947 standard; protein; 425 AA.
DE E. faecium protein sequence SEQ ID 6574.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 7; Length 425;
Best Local Similarity 25.9%; Pred. No. 65;
RESULT 1176
ID ADA34110 standard; protein; 470 AA.
DE Acinetobacter baumannii protein #1271.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 470;
Best Local Similarity 23.5%; Pred. No. 74;
RESULT 1177
ID ABM67264 standard; protein; 474 AA.
DE Photorhabdus luminescens protein sequence #361.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 6; Length 474;
Best Local Similarity 22.9%; Pred. No. 75;
RESULT 1178
ID AAE16787 standard; protein; 475 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 475;
Best Local Similarity 25.0%; Pred. No. 76;
RESULT 1179

ID ADA89683 standard; protein; 506 AA.
DE Staphylococcus aureus antigenic protein #222.
PN WO2003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 82;
RESULT 1180
ID AEW72414 standard; protein; 506 AA.
DE Staphylococcus aureus protein #1654.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 82;
RESULT 1181
ID AAE21176 standard; protein; 540 AA.
DE Human TRICH-A20 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 540;
Best Local Similarity 25.0%; Pred. No. 90;
RESULT 1182
ID AAM39017 standard; protein; 552 AA.
DE Human polypeptide SEQ ID NO 2162.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 4; Length 552;
Best Local Similarity 25.0%; Pred. No. 93;
RESULT 1183
ID ABU18262 standard; protein; 602 AA.
DE Protein encoded by Prokaryotic essential gene #3789.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 602;
Best Local Similarity 26.4%; Pred. No. 1e+02;
RESULT 1184
ID ABU33453 standard; protein; 637 AA.
DE Protein encoded by Prokaryotic essential gene #18980.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 637;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 1185
ID AAY91335 standard; protein; 640 AA.
DE Group B Streptococcus protein sequence SEQ ID NO:68.
PN WO200006736-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNICS LTD.
Query Match 5.9%; Score 70; DB 3; Length 640;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1186
ID ADL04660 standard; protein; 767 AA.
DE M. catarrhalis protein #426.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 767;
Best Local Similarity 21.3%; Pred. No. 1.5e+02;
RESULT 1187
ID AAR53921 standard; protein; 980 AA.
DE HCV fusion protein corresp. to N-terminal of ORF.
PN JP06092996-A.
PD 05-APR-1994.
PA (SHIM/) SHIMOTOYA K.
Query Match 5.9%; Score 70; DB 2; Length 980;
Best Local Similarity 24.6%; Pred. No. 2.1e+02;
RESULT 1188

ID ADP07803 standard; protein; 138 AA.
DE Human secreted protein, seq id 286.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 8; Length 138;
Best Local Similarity 22.0%; Pred. No. 16;
RESULT 1189
ID ADA33664 standard; protein; 198 AA.
DE Acinetobacter baumannii protein #825.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 198;
Best Local Similarity 23.3%; Pred. No. 26;
RESULT 1190
ID ADB09276 standard; protein; 201 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 201;
Best Local Similarity 26.0%; Pred. No. 26;
RESULT 1191
ID AAU29449 standard; protein; 210 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #70.
PN WO200168858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 69.5; DB 4; Length 210;
Best Local Similarity 20.9%; Pred. No. 28;
RESULT 1192
ID AEG60737 standard; protein; 210 AA.
DE Novel G protein coupled receptor (nGCPR-x) #70.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 5.8%; Score 69.5; DB 5; Length 210;
Best Local Similarity 20.9%; Pred. No. 28;
RESULT 1193
ID AAU01288 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN WO200125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 29;
RESULT 1194
ID ADB09278 standard; protein; 247 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3218.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 247;
Best Local Similarity 26.0%; Pred. No. 35;
RESULT 1195
ID AEG66935 standard; protein; 253 AA.
DE Novel G-protein coupled receptor related protein #12.
PN WO200240539-A2.
PD 23-MAY-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 253;
Best Local Similarity 24.2%; Pred. No. 36;
RESULT 1196
ID ABB62542 standard; protein; 261 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 261;
Best Local Similarity 27.7%; Pred. No. 38;
RESULT 1197
ID ABO80446 standard; protein; 270 AA.

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DE Pseudomonas aeruginosa polypeptide #12621.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match 5.8%; Score 69.5; DB 7; Length 270;
  Best Local Similarity 22.1%; Pred. No. 40;
RESULT 1198
ID ADE86076 standard; protein; 296 AA.
DE Streptomyces hygroscopicus ABC transporter.
PN WO2003082909-A1.
PD 09-OCT-2003.
PA (AMHP ) WYETH.
  Query Match 5.8%; Score 69.5; DB 7; Length 296;
  Best Local Similarity 21.0%; Pred. No. 45;
RESULT 1199
ID RAG71524 standard; protein; 308 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
  Query Match 5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1200
ID ABB4525 standard; protein; 308 AA.
DE Human GPCR3 polypeptide SEQ ID NO 9.
PN WO200174904-A2.
PD 11-OCT-2001.
PA (CURA-) CURAGEN CORP.
  Query Match 5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1201
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLF242.
PN WO200168805-A2.
PD 20-SEP-2001.
PA (SENO-) SENOMYX INC.
  Query Match 5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1202
ID ABP95703 standard; protein; 308 AA.
DE Human GPCR polypeptide SEQ ID NO 216.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
  Query Match 5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1203
ID AAU95729 standard; protein; 308 AA.
DE Human olfactory and pheromone G protein-coupled receptor #216.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEWCOM SA.
  Query Match 5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1204
ID AAU85362 standard; protein; 308 AA.
DE G-coupled olfactory receptor #223.
PN WO200198526-A2.
PD 27-DEC-2001.
PA (SENO-) SENOMYX INC.
  Query Match 5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1205
ID ADC86333 standard; protein; 308 AA.
DE Human GPCR protein SEQ ID NO:786.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
  Query Match 5.8%; Score 69.5; DB 7; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1206
DE Rat Sprague-Dawley putative GCR polypeptide.
ID ADH10684 standard; protein; 354 AA.
DE Rat Sprague-Dawley putative GCR polypeptide.
ID ABW2126 standard; protein; 308 AA.
DE Human GPCR3 protein.
PN US2003195335-A1.
PD 16-OCT-2003.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (CASM/) CASMAN S.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (PADI/) PADIGARU M.
PA (TAYL/) TAYLOR S.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S.
PA (KERU/) KERUDA R.
PA (GANG/) GANGOLLI E A.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (MACD/) MACDOUGALL J R.
  Query Match 5.8%; Score 69.5; DB 7; Length 308;
  Best Local Similarity 20.9%; Pred. No. 47;
RESULT 1207
ID ABR01671 standard; protein; 316 AA.
DE Human G protein coupled receptor SEQ ID 202.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
  Query Match 5.8%; Score 69.5; DB 6; Length 316;
  Best Local Similarity 20.9%; Pred. No. 49;
RESULT 1208
ID AAY35360 standard; protein; 321 AA.
DE Chlamydia pneumoniae involved in the virulence process.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST ) GENSET.
  Query Match 5.8%; Score 69.5; DB 2; Length 321;
  Best Local Similarity 21.4%; Pred. No. 50;
RESULT 1209
ID ADC33485 standard; protein; 321 AA.
DE Yeast ARV1.
PN US6566512-B1.
PD 20-MAY-2003.
PA (UYCO ) UNIV COLUMBIA NEW YORK.
  Query Match 5.8%; Score 69.5; DB 7; Length 321;
  Best Local Similarity 18.8%; Pred. No. 50;
RESULT 1210
ID ADE37749 standard; protein; 321 AA.
DE Yeast ARV1 (ARS-2 Required for viability).
PN US2003186879-A1.
PD 02-OCT-2003.
PA (UYCO ) UNIV COLUMBIA NEW YORK.
  Query Match 5.8%; Score 69.5; DB 7; Length 321;
  Best Local Similarity 18.8%; Pred. No. 50;
RESULT 1211
ID AAU53139 standard; protein; 327 AA.
DE Propionibacterium acnes immunogenic protein #14035.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
  Query Match 5.8%; Score 69.5; DB 4; Length 327;
  Best Local Similarity 25.5%; Pred. No. 52;
RESULT 1212
ID ABW49658 standard; protein; 327 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
  Query Match 5.8%; Score 69.5; DB 6; Length 327;
  Best Local Similarity 25.5%; Pred. No. 52;
RESULT 1213
ID ADH10684 standard; protein; 354 AA.
DE Rat Sprague-Dawley putative GCR polypeptide.

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PN WO2003104484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.8%; Score 69.5; DB 8; Length 354;
Best Local Similarity 22.0%; Pred. No. 58;
RESULT 1214
ID AAY05489 standard; protein; 382 AA.
DE Human EDG-2 protein sequence.
PN WO9919513-A2.
PD 22-APR-1999.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match 5.8%; Score 69.5; DB 2; Length 382;
Best Local Similarity 20.2%; Pred. No. 64;
RESULT 1215
ID AAU0302 standard; protein; 382 AA.
DE LPA receptor-related amino acid sequence #1.
PN WO200112838-A2.
PD 22-FEB-2001.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match 5.8%; Score 69.5; DB 4; Length 382;
Best Local Similarity 20.2%; Pred. No. 64;
RESULT 1216
ID ABG76099 standard; protein; 382 AA.
DE Human lysophosphatidic acid (LPA) receptor EDG-1.
PN US6485922-B1.
PD 26-NOV-2002.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match 5.8%; Score 69.5; DB 6; Length 382;
Best Local Similarity 20.2%; Pred. No. 64;
RESULT 1217
ID ABB47613 standard; protein; 400 AA.
DE Listeria monocytogenes protein #317.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 400;
Best Local Similarity 22.9%; Pred. No. 68;
RESULT 1218
ID ABU32698 standard; protein; 400 AA.
DE Protein encoded by Prokaryotic essential gene #18225.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 400;
Best Local Similarity 22.9%; Pred. No. 68;
RESULT 1219
ID ADL12060 standard; protein; 401 AA.
DE Drosophila dmt1p1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 401;
Best Local Similarity 20.9%; Pred. No. 68;
RESULT 1220
ID ABB60948 standard; protein; 415 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 415;
Best Local Similarity 20.9%; Pred. No. 72;
RESULT 1221
ID ADL12059 standard; protein; 415 AA.
DE Drosophila dmt1p2 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 415;
Best Local Similarity 20.9%; Pred. No. 72;
RESULT 1222
ID ABB66992 standard; protein; 428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 428;
Best Local Similarity 20.9%; Pred. No. 75;
RESULT 1223
ID ADL12058 standard; protein; 428 AA.
DE Drosophila dmt1p1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 428;
Best Local Similarity 20.9%; Pred. No. 75;
RESULT 1224
ID AAY41284 standard; protein; 444 AA.
DE ci-NT-his fusion protein encoded by plasmid pLJM6-09.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 444;
Best Local Similarity 23.6%; Pred. No. 79;
RESULT 1225
ID AAG30875 standard; protein; 453 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 453;
Best Local Similarity 23.3%; Pred. No. 81;
RESULT 1226
ID ADK47327 standard; protein; 453 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3842.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 453;
Best Local Similarity 24.4%; Pred. No. 81;
RESULT 1227
ID AAG30874 standard; protein; 476 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 476;
Best Local Similarity 23.3%; Pred. No. 87;
RESULT 1228
ID ABO61637 standard; protein; 494 AA.
DE Klebsiella pneumoniae polypeptide seqid 8154.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 494;
Best Local Similarity 22.0%; Pred. No. 91;
RESULT 1229
ID AAY41278 standard; protein; 500 AA.
DE Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 500;
Best Local Similarity 23.6%; Pred. No. 93;
RESULT 1230
ID AAG30873 standard; protein; 503 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 503;
Best Local Similarity 23.3%; Pred. No. 94;
RESULT 1231
ID AAY92829 standard; protein; 535 AA.
DE C. pneumoniae CPN100557 processed antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity 21.4%; Pred. No. 1e+02;

RESULT 1232
ID AAY92828 standard; protein; 547 AA.
DE C. pneumoniae CPN100557 antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1233
ID ABU26764 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #12291.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1234
ID ABU31940 standard; protein; 551 AA.
DE Protein encoded by Prokaryotic essential gene #17467.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 551;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1235
ID AAY01650 standard; protein; 557 AA.
DE A protein with cation transporting activity.
PN WO9913072-A1.
PD 18-MAR-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1236
ID RAY83929 standard; protein; 557 AA.
DE Human carnitine transporter protein OCTN2.
PN WO200014210-A1.
PD 16-MAR-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1237
ID ABG03029 standard; protein; 557 AA.
DE Novel human diagnostic protein #3020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1238
ID ABB82979 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN WO20029053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1239
ID ABB82980 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN WO20029053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1240
ID ABO07242 standard; protein; 557 AA.
DE Human p53 modifying protein, SEQ ID 202.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1241
ID ADE09321 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #387.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1242
ID ADE09261 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #327.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1243
ID ADA34637 standard; protein; 559 AA.
DE Acinetobacter baumannii protein #1798.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 559;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1244
ID ABO62908 standard; protein; 564 AA.
DE Klebsiella pneumoniae polypeptide seqid 9425.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity 23.6%; Pred. No. 1.1e+02;
RESULT 1245
ID ABB89665 standard; protein; 568 AA.
DE Human polypeptide SEQ ID NO 2041.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
RESULT 1246
ID ADB65515 standard; protein; 573 AA.
DE Human protein encoded by clone TESTI20271790.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 5.8%; Score 69.5; DB 7; Length 573;
Best Local Similarity 22.7%; Pred. No. 1.1e+02;
RESULT 1247
ID ABB47410 standard; protein; 579 AA.
DE Listeria monocytogenes protein #114.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.1e+02;
RESULT 1248
ID ABU32703 standard; protein; 579 AA.
DE Protein encoded by Prokaryotic essential gene #18230.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.1e+02;
RESULT 1249
ID ABP65234 standard; protein; 599 AA.
DE Hypoxia-regulated protein #108.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.8%; Score 69.5; DB 5; Length 599;
Best Local Similarity 19.8%; Pred. No. 1.2e+02;
RESULT 1250

ID AAE3584 standard; protein; 599 AA.
DE Human GAT1 GABA transporter protein.
PN WO2003061573-A2.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.2e+02;
RESULT 1251
ID ADD46025 standard; protein; 599 AA.
DE Human Protein P30531, SEQ ID NO 11697.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.2e+02;
RESULT 1252
ID AAY41285 standard; protein; 656 AA.
DE CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UVVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 656;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1253
ID ABP40194 standard; protein; 660 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1254
ID AAY17390 standard; protein; 663 AA.
DE Human vesicle membrane protein-like protein 3.
PN WO9921994-A2.
PD 06-MAY-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69.5; DB 2; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1255
ID ADM83092 standard; protein; 663 AA.
DE Human vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1256
ID ADJ64317 standard; protein; 663 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 12.
PN WO2004013326-A1.
PD 12-FEB-2004.
PA (ASAH) ASAHI KASEI KK.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1257
ID ADO09827 standard; protein; 681 AA.
DE Hamster SGLT homologue protein SEQ ID NO:50.
PN WO2004039405-A1.
PD 13-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69.5; DB 8; Length 681;
Best Local Similarity 24.5%; Pred. No. 1.4e+02;
RESULT 1258
ID ABU41908 standard; protein; 695 AA.
DE Protein encoded by Prokaryotic essential gene #27435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 695;
Best Local Similarity 24.3%; Pred. No. 1.5e+02;
RESULT 1259

ID ADJ48367 standard; protein; 764 AA.
DE Maize oil-associated gene protein #26.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.8%; Score 69.5; DB 8; Length 764;
Best Local Similarity 21.0%; Pred. No. 1.7e+02;
RESULT 1260
ID ABU43821 standard; protein; 801 AA.
DE Protein encoded by Prokaryotic essential gene #29348.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 801;
Best Local Similarity 19.9%; Pred. No. 1.8e+02;
RESULT 1261
ID AAY70245 standard; protein; 805 AA.
DE Human Polycystin-L protein.
PN WO200012048-A2.
PD 09-MAR-2000.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 5.8%; Score 69.5; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 1.8e+02;
RESULT 1262
ID ABB98140 standard; protein; 863 AA.
DE Human PMW incyte ID 7484157CD1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 69.5; DB 5; Length 863;
Best Local Similarity 19.3%; Pred. No. 2e+02;
RESULT 1263
ID AAY96168 standard; protein; 877 AA.
DE Saccharomyces cerevisiae OPT protein YPR194C.
PN WO200052162-A2.
PD 08-SEP-2000.
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (BECK/) BECKER J M.
PA (HAUS/) HAUSER M.
PA (DONH/) DONHARDT A.
PA (BARN/) BARNES D.
Query Match 5.8%; Score 69.5; DB 3; Length 877;
Best Local Similarity 22.7%; Pred. No. 2e+02;
RESULT 1264
ID AAG70761 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL197W.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.8%; Score 69.5; DB 4; Length 881;
Best Local Similarity 24.4%; Pred. No. 2e+02;
RESULT 1265
ID ABU16635 standard; protein; 1010 AA.
DE Protein encoded by Prokaryotic essential gene #2162.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 1010;
Best Local Similarity 24.7%; Pred. No. 2.5e+02;
RESULT 1266
ID ADA34462 standard; protein; 1028 AA.
DE Acinetobacter baumannii protein #1623.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 1028;
Best Local Similarity 24.7%; Pred. No. 2.5e+02;
RESULT 1267
ID AAW25671 standard; protein; 1684 AA.

DE hABC3 protein.
 PN WO9702346-A2.
 PD 23-JAN-1997.
 PA (GENZ) GENZYME CORP.
 Query Match 5.8%; Score 69.5; DB 2; Length 1684;
 Best Local Similarity 20.3%; Pred. No. 5e+02;
 RESULT 1268
 ID AAW46761 standard; protein; 1684 AA.
 DE Amino acid sequence of human ATP binding cassette transporter.
 PN WO9748797-A1.
 PD 24-DEC-1997.
 PA (GENZ) GENZYME CORP.
 Query Match 5.8%; Score 69.5; DB 2; Length 1684;
 Best Local Similarity 20.3%; Pred. No. 5e+02;
 RESULT 1269
 ID AAW46771 standard; protein; 1704 AA.
 DE Amino acid sequence of human ATP binding cassette transporter.
 PN WO9748797-A1.
 PD 24-DEC-1997.
 PA (GENZ) GENZYME CORP.
 Query Match 5.8%; Score 69.5; DB 2; Length 1704;
 Best Local Similarity 20.3%; Pred. No. 5.1e+02;
 RESULT 1270
 ID ABP52094 standard; protein; 1704 AA.
 DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
 PN EP1217066-A1.
 PD 26-JUN-2002.
 PA (UYGE-) UNIV GENT.
 Query Match 5.8%; Score 69.5; DB 5; Length 1704;
 Best Local Similarity 20.3%; Pred. No. 5.1e+02;
 RESULT 1271
 ID ADJ70414 standard; protein; 1704 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID2220.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.8%; Score 69.5; DB 7; Length 1704;
 Best Local Similarity 20.3%; Pred. No. 5.1e+02;
 RESULT 1272
 ID ADL61289 standard; protein; 1704 AA.
 DE Human ATP-binding cassette subfamily A (ABCL) member 3 protein.
 PN WO2004020583-A2.
 PD 11-MAR-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 5.8%; Score 69.5; DB 8; Length 1704;
 Best Local Similarity 20.3%; Pred. No. 5.1e+02;
 RESULT 1273
 ID ADB09274 standard; protein; 154 AA.
 DE Alloiococcus otitis antigenic protein SEQ ID NO:3214.
 PN WO2003048304-A2.
 PD 12-JUN-2003.
 PA (AMHP) WYETH HOLDINGS CORP.
 Query Match 5.8%; Score 69; DB 6; Length 154;
 Best Local Similarity 27.3%; Pred. No. 21;
 RESULT 1274
 ID ADK16543 standard; protein; 178 AA.
 DE Nanoarchaeum equitans cancer-associated (CA) protein #247.
 PN WO2003093434-A2.
 PD 13-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 5.8%; Score 69; DB 8; Length 178;
 Best Local Similarity 23.3%; Pred. No. 25;
 RESULT 1275
 ID AAU65589 standard; protein; 191 AA.
 DE Propionibacterium acnes immunogenic protein #26485.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69; DB 4; Length 191;
 Best Local Similarity 26.6%; Pred. No. 28;
 RESULT 1276
 ID ABM62108 standard; protein; 191 AA.
 DE Propionibacterium acnes permease/transporter-related polypeptide #26784.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69; DB 6; Length 191;
 Best Local Similarity 26.6%; Pred. No. 28;
 RESULT 1277
 ID AAW38633 standard; protein; 193 AA.
 DE S. pneumoniae LPLC protein.
 PN WO9743303-A1.
 PD 20-NOV-1997.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 5.8%; Score 69; DB 2; Length 193;
 Best Local Similarity 28.3%; Pred. No. 28;
 RESULT 1278
 ID AAB21047 standard; protein; 214 AA.
 DE Human nucleic acid-binding protein, NuABP-51.
 PN WO200044900-A2.
 PD 03-AUG-2000.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 5.8%; Score 69; DB 3; Length 214;
 Best Local Similarity 24.7%; Pred. No. 33;
 RESULT 1279
 ID ABP58238 standard; protein; 214 AA.
 DE Human ovary-specific OI-236 (NPW2) protein.
 PN WO200288314-A2.
 PD 07-NOV-2002.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (AMHP) WYETH.
 Query Match 5.8%; Score 69; DB 6; Length 214;
 Best Local Similarity 24.7%; Pred. No. 33;
 RESULT 1280
 ID ADJ63172 standard; protein; 214 AA.
 DE Human nucleoplasmin (Npm2) protein.
 PN WO2003091400-A2.
 PD 08-NOV-2003.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (AMHP) WYETH.
 Query Match 5.8%; Score 69; DB 7; Length 214;
 Best Local Similarity 24.7%; Pred. No. 33;
 RESULT 1281
 ID ADM03849 standard; protein; 214 AA.
 DE Human protein of the invention SEQ ID NO:2534.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.8%; Score 69; DB 7; Length 214;
 Best Local Similarity 24.7%; Pred. No. 33;
 RESULT 1282
 ID ADN46858 standard; protein; 239 AA.
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID736.
 PN WO2004022736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 5.8%; Score 69; DB 8; Length 239;
 Best Local Similarity 23.5%; Pred. No. 38;
 RESULT 1283
 ID ABM69545 standard; protein; 337 AA.
 DE Photorhabdus luminescens protein sequence #2642.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 5.8%; Score 69; DB 6; Length 337;
 Best Local Similarity 19.8%; Pred. No. 62;
 RESULT 1284
 ID ABM72781 standard; protein; 350 AA.
 DE Staphylococcus aureus protein #2021.
 PN WO200294868-A2.
 PD 28-NOV-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 5.8%; Score 69; DB 6; Length 350;

Best Local Similarity 20.5%; Pred. No. 65;
RESULT 1285
ID AAG04120 standard; protein; 356 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 356;
Best Local Similarity 21.0%; Pred. No. 66;
RESULT 1286
ID AAR91218 standard; protein; 370 AA.
DE Human pituitary G-protein coupled receptor protein.
PN W09605302-A1.
PD 22-FEB-1996.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1287
ID AAW31379 standard; protein; 370 AA.
DE Human G-protein-coupled receptor protein from phGR3.
PN W09724438-A2.
PD 10-JUL-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1288
ID AAW95181 standard; peptide; 370 AA.
DE Human G-protein coupled receptor polypeptide.
PN W09849295-A1.
PD 05-NOV-1998.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1289
ID AAW97221 standard; peptide; 370 AA.
DE Human pituitary-derived G protein-coupled receptor protein.
PN W09859962-A1.
PD 30-DEC-1998.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1290
ID AAG04119 standard; protein; 370 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 370;
Best Local Similarity 21.0%; Pred. No. 70;
RESULT 1291
ID AAG62539 standard; protein; 370 AA.
DE Human CRH releasing protein related protein SEQ ID NO: 46.
PN W0200135984-A1.
PD 25-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 4; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1292
ID ABP81880 standard; protein; 370 AA.
DE Human G-protein-coupled receptor 10 protein SEQ ID NO: 245.
PN W0200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.8%; Score 69; DB 6; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1293
ID ADO29365 standard; protein; 370 AA.
DE Human GPCR GPR10, SEQ ID NO: 466.
PN W02004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.8%; Score 69; DB 8; Length 370;
Best Local Similarity 21.8%; Pred. No. 70;
RESULT 1294
ID AAW27510 standard; protein; 380 AA.
DE Consensus human hypothalamic receptor.
PN W09708317-A2.
PD 06-MAR-1997.
PA (CHIR) CHIRON CORP.
Query Match 5.8%; Score 69; DB 2; Length 380;
Best Local Similarity 21.8%; Pred. No. 73;
RESULT 1295
ID AAB16020 standard; protein; 388 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO: 378.
PN W0200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 3; Length 388;
Best Local Similarity 27.2%; Pred. No. 75;
RESULT 1296
ID AAG98322 standard; protein; 388 AA.
DE Escherichia coli protein sequence SEQ ID NO: 370.
PN W0200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 4; Length 388;
Best Local Similarity 27.2%; Pred. No. 75;
RESULT 1297
ID ABU14818 standard; protein; 388 AA.
DE Protein encoded by Prokaryotic essential gene #345.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 6; Length 388;
Best Local Similarity 27.2%; Pred. No. 75;
RESULT 1298
ID ABO61901 standard; protein; 472 AA.
DE Klebsiella pneumoniae polypeptide seqid 8418.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 472;
Best Local Similarity 21.3%; Pred. No. 98;
RESULT 1299
ID AAG42138 standard; protein; 508 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52514.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 508;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1300
ID AAG04118 standard; protein; 509 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 509;
Best Local Similarity 21.0%; Pred. No. 1.1e+02;
RESULT 1301
ID AAG42137 standard; protein; 520 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52513.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 520;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1302
ID ABB59760 standard; protein; 593 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6072.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69; DB 4; Length 593;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1303
ID AAG31959 standard; protein; 609 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38469.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 609;

Best Local Similarity 21.0%; Pred. No. 1.4e+02;
RESULT 1304
ID AAG31958 standard; protein; 624 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38468.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 624;
Best Local Similarity 21.0%; Pred. No. 1.4e+02;
RESULT 1305
ID AAE05101 standard; protein; 641 AA.
DE Drosophila melanogaster dmKSNP.
PN WO200149848-A2.
PD 12-JUL-2001.
PA (GENO-) GENOPTERA LLC.
Query Match 5.8%; Score 69; DB 4; Length 641;
Best Local Similarity 22.7%; Pred. No. 1.5e+02;
RESULT 1306
ID AAG31957 standard; protein; 659 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38467.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 659;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 1307
ID ABB11769 standard; peptide; 666 AA.
DE Human dU37C10.3 ATPase homologue, SEQ ID NO: 21139.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.6e+02;
RESULT 1308
ID AAM79751 standard; protein; 666 AA.
DE Human protein SEQ ID NO 3397.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.6e+02;
RESULT 1309
ID ADF05168 standard; protein; 681 AA.
DE Bacterial polypeptide #1281.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 681;
Best Local Similarity 21.5%; Pred. No. 1.6e+02;
RESULT 1310
ID ABO52988 standard; protein; 791 AA.
DE Human putative spliceosome associated protein (SAP) #52.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 5.8%; Score 69; DB 6; Length 791;
Best Local Similarity 24.8%; Pred. No. 2e+02;
RESULT 1311
ID AAB42779 standard; protein; 792 AA.
DE Human ORF2543 polypeptide sequence SEQ ID NO: 5086.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69; DB 3; Length 792;
Best Local Similarity 24.8%; Pred. No. 2e+02;
RESULT 1312
ID ABP62960 standard; protein; 875 AA.
DE Human polypeptide SEQ ID NO 397.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 5; Length 875;
Best Local Similarity 24.8%; Pred. No. 2.3e+02;
RESULT 1313

ID ABB90877 standard; protein; 1933 AA.
DE Herbicidally active polypeptide SEQ ID NO 88.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69; DB 5; Length 1933;
Best Local Similarity 17.4%; Pred. No. 6.9e+02;
RESULT 1314
ID ADM68764 standard; protein; 5127 AA.
DE Peregrinus maidis ryanodine receptor protein SEQ ID NO: 8.
PN WO2004027042-A2.
PD 01-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.8%; Score 69; DB 8; Length 5127;
Best Local Similarity 20.1%; Pred. No. 2.7e+03;
RESULT 1315
ID ADH5829 standard; protein; 178 AA.
DE Enterococcus faecalis polypeptide #309.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.7%; Score 68.5; DB 7; Length 178;
Best Local Similarity 30.7%; Pred. No. 29;
RESULT 1316
ID ABU01003 standard; protein; 209 AA.
DE Human breast specific protein SEQ ID NO: 86.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 5.7%; Score 68.5; DB 5; Length 209;
Best Local Similarity 21.8%; Pred. No. 36;
RESULT 1317
ID AAG53772 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68492.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 39;
RESULT 1318
ID AAG25640 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29784.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 39;
RESULT 1319
ID AAG53747 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 39;
RESULT 1320
ID ADF07413 standard; protein; 225 AA.
DE Bacterial polypeptide #3526.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 225;
Best Local Similarity 18.2%; Pred. No. 40;
RESULT 1321
ID ADO57686 standard; protein; 227 AA.
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide #68.
PN WO2004045499-A2.
PD 03-JUN-2004.
PA (UYFL) UNIV FLORIDA.
Query Match 5.7%; Score 68.5; DB 8; Length 227;
Best Local Similarity 24.3%; Pred. No. 41;
RESULT 1322
ID ADA14398 standard; protein; 278 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO: 140.
PN WO2003068969-A1.

PD 21-AUG-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 5.7%; Score 68.5; DB 6; Length 278;
 Best Local Similarity 29.2%; Pred. No. 54;
 RESULT 1323
 ID ABU29281 standard; protein; 322 AA.
 DE Protein encoded by Prokaryotic essential gene #14808.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.7%; Score 68.5; DB 6; Length 322;
 Best Local Similarity 30.7%; Pred. No. 66;
 RESULT 1324
 ID AB99751 standard; protein; 327 AA.
 DE Amino acid sequence of bacteriophage phiCpln antigenic protein.
 PN WO200295413-A2.
 PD 28-NOV-2002.
 PA (UVBR-) UNIV BRITISH COLUMBIA.
 Query Match 5.7%; Score 68.5; DB 6; Length 327;
 Best Local Similarity 27.0%; Pred. No. 68;
 RESULT 1325
 ID AAW25926 standard; protein; 354 AA.
 DE Xenopus melatonin receptor MEL-1Aa.
 PN WO9704094-A1.
 PD 06-FEB-1997.
 PA (ADIR-) ADIR & CIE.
 Query Match 5.7%; Score 68.5; DB 2; Length 354;
 Best Local Similarity 18.8%; Pred. No. 75;
 RESULT 1326
 ID AAY87506 standard; protein; 369 AA.
 DE Human G coupled-protein receptor, GPR10.
 PN WO200017641-A1.
 PD 30-MAR-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 5.7%; Score 68.5; DB 3; Length 369;
 Best Local Similarity 23.3%; Pred. No. 80;
 RESULT 1327
 ID AAE13430 standard; protein; 377 AA.
 DE Brassica napus microsomal omega-3 desaturase, bnFAD3 protein.
 PN WO200179499-A1.
 PD 25-OCT-2001.
 PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
 Query Match 5.7%; Score 68.5; DB 4; Length 377;
 Best Local Similarity 29.3%; Pred. No. 82;
 RESULT 1328
 ID AAB28521 standard; protein; 382 AA.
 DE Mouse EDG1 polypeptide.
 PN WO200059529-A1.
 PD 12-OCT-2000.
 PA (SMIK-) SMITHKLINE BEECHAM CORP.
 Query Match 5.7%; Score 68.5; DB 3; Length 382;
 Best Local Similarity 19.8%; Pred. No. 84;
 RESULT 1329
 ID ADO29286 standard; protein; 382 AA.
 DE Mouse GPCR EDG1, SEQ ID NO:387.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 PA (PRIM-) PRIMAL INC.
 Query Match 5.7%; Score 68.5; DB 8; Length 382;
 Best Local Similarity 19.8%; Pred. No. 84;
 RESULT 1330
 ID AAW01664 standard; protein; 383 AA.
 DE p(rat-edg), G-protein coupled receptor.
 PN US5585476-A.
 PD 17-DEC-1996.
 PA (MACL/) MACLENNAN A J.
 Query Match 5.7%; Score 68.5; DB 2; Length 383;
 Best Local Similarity 19.8%; Pred. No. 84;
 RESULT 1331
 ID AAW87791 standard; protein; 383 AA.
 DE Rat-edg, G-protein coupled receptor superfamily member.
 PN US5856443-A.
 PD 03-JAN-1999.

PA (MACL/) MACLENNAN A J.
 Query Match 5.7%; Score 68.5; DB 2; Length 383;
 Best Local Similarity 19.8%; Pred. No. 84;
 RESULT 1332
 ID ABU61817 standard; protein; 383 AA.
 DE Rat-edg.
 PN US6518414-B1.
 PD 11-FEB-2003.
 PA (MACL/) MACLENNAN A J.
 Query Match 5.7%; Score 68.5; DB 7; Length 383;
 Best Local Similarity 19.8%; Pred. No. 84;
 RESULT 1333
 ID AEG07020 standard; protein; 404 AA.
 DE Novel human diagnostic protein #7011.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.7%; Score 68.5; DB 4; Length 404;
 Best Local Similarity 22.4%; Pred. No. 91;
 RESULT 1334
 ID AAB68619 standard; protein; 411 AA.
 DE Human PAC 1 receptor isoform 30.
 PN WO200107478-A1.
 PD 01-FEB-2001.
 PA (MEDI-) MEDICAL RES COUNCIL.
 Query Match 5.7%; Score 68.5; DB 4; Length 411;
 Best Local Similarity 29.9%; Pred. No. 93;
 RESULT 1335
 ID ADH87117 standard; protein; 417 AA.
 DE Enterococcus faecalis polypeptide #1597.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 5.7%; Score 68.5; DB 7; Length 417;
 Best Local Similarity 23.2%; Pred. No. 95;
 RESULT 1336
 ID AAR88409 standard; protein; 420 AA.
 DE High-affinity melatonin receptor.
 PN WO9535320-A1.
 PD 28-DEC-1995.
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
 Query Match 5.7%; Score 68.5; DB 2; Length 420;
 Best Local Similarity 18.8%; Pred. No. 96;
 RESULT 1337
 ID AAW88344 standard; protein; 430 AA.
 DE Salmonella enterica O antigen pathway flippase protein.
 PN WO9850531-A1.
 PD 12-NOV-1998.
 PA (UNSY) UNIV SYDNEY.
 Query Match 5.7%; Score 68.5; DB 2; Length 430;
 Best Local Similarity 23.6%; Pred. No. 99;
 RESULT 1338
 ID AAU02941 standard; protein; 431 AA.
 DE Angiotensin converting enzyme (ACEV) splice variant protein #41.
 PN WO200136632-A2.
 PD 25-MAY-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match 5.7%; Score 68.5; DB 4; Length 431;
 Best Local Similarity 29.9%; Pred. No. 99;
 RESULT 1339
 ID ADA33815 standard; protein; 437 AA.
 DE Acinetobacter baumannii protein #976.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.7%; Score 68.5; DB 6; Length 437;
 Best Local Similarity 20.5%; Pred. No. 16+02;
 RESULT 1340
 ID AAB71866 standard; protein; 444 AA.
 DE Human CSF1 seven transmembrane domain.
 PN WO200109328-A1.
 PD 08-FEB-2001.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1341
ID AAE26685 standard; protein; 444 AA.
DE Human CRF-RA2 splice variant protein.
PN US2002055617-A1.
PD 09-MAY-2002.
PA (PERR/) FERRIN M H.
PA (CHEN/) CHEN R.
PA (LEWIS/) LEWIS K A.
PA (VALE/) VALE W W.
PA (DONA/) DONALDSON C J.
PA (SAWC/) SAWCHENKO P.
Query Match 5.7%; Score 68.5; DB 5; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1342
ID ABR43052 standard; protein; 444 AA.
DE Human CRH-R1 beta protein SEQ ID NO:2.
PN WO2003024990-A2.
PD 27-MAR-2003.
PA (UYTE-) UNIV TENNESSEE RES CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1343
ID ABU08081 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor 2 (CRF-R2).
PN US6495343-B1.
PD 17-DEC-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1344
ID ABG76402 standard; protein; 444 AA.
DE Human hCRF-RAL, splice variant.
PN US6482608-B1.
PD 19-NOV-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1345
ID ADE62734 standard; protein; 444 AA.
DE Human Protein P34998, SEQ ID NO 8667.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 68.5; DB 7; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1346
ID ADJ65810 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor CRF-RA2.
PN US2004039173-A1.
PD 26-FEB-2004.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 8; Length 444;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1347
ID ADC86255 standard; protein; 447 AA.
DE Human GPCR protein SEQ ID NO:708.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 447;
Best Local Similarity 23.7%; Pred. No. 1e+02;
RESULT 1348
ID AAR58668 standard; protein; 448 AA.
DE Human PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 448;
Best Local Similarity 23.7%; Pred. No. 1e+02;

Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 1349
ID ABB56380 standard; protein; 468 AA.
DE Non-endogenous human GPCR protein, SEQ ID NO: 553.
PN WO200177172-A2.
PD 18-OCT-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1350
ID AAB71874 standard; protein; 468 AA.
DE Human PACR seven transmembrane domain.
PN WO200109328-A1.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1351
ID ADC86185 standard; protein; 468 AA.
DE Human GPCR protein SEQ ID NO:638.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1352
ID ADO29153 standard; protein; 468 AA.
DE Human GPCR ADCYAP1R1, SEQ ID NO:254.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 68.5; DB 8; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1353
ID AAR58670 standard; protein; 475 AA.
DE Human PACAP receptor type 1-B2 mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 475;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1354
ID AAR58671 standard; protein; 476 AA.
DE Human PACAP receptor type 1C mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1355
ID AAR58669 standard; protein; 476 AA.
DE Human PACAP receptor type 1B mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1356
ID ABP65829 standard; protein; 495 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 5.7%; Score 68.5; DB 5; Length 495;
Best Local Similarity 28.6%; Pred. No. 1.2e+02;
RESULT 1357
ID AAB68618 standard; protein; 524 AA.
DE Human PAC 1 receptor.
PN WO200107478-A1.
PD 01-FEB-2001.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 5.7%; Score 68.5; DB 4; Length 524;

Best Local Similarity 29.9%; Pred. No. 1.3e+02;
RESULT 1358
ID AAR58659 standard; protein; 525 AA.
DE Human PACAP receptor type 1A protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.3e+02;
RESULT 1359
ID AEU08611 standard; protein; 525 AA.
DE Human pituitary adenylate cyclase (PAC) 1 receptor.
PN US2002182729-A1.
PD 05-DEC-2002.
PA (DICI/) DICICCO-BLOOM E.
PA (NICO/) NICOT A.
PA (LUNN/) LU N.
PA (SUHJ/) SUH J.
Query Match 5.7%; Score 68.5; DB 6; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.3e+02;
RESULT 1360
ID ABF81873 standard; protein; 525 AA.
DE Human PACAP receptor type 1 protein SEQ ID NO:231.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.7%; Score 68.5; DB 6; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.3e+02;
RESULT 1361
ID ADN38958 standard; protein; 525 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.7%; Score 68.5; DB 7; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.3e+02;
RESULT 1362
ID ABF73995 standard; protein; 541 AA.
DE Candida albicans essential protein SEQ ID NO 7832.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 5; Length 541;
Best Local Similarity 21.7%; Pred. No. 1.4e+02;
RESULT 1363
ID ABG95329 standard; protein; 548 AA.
DE Human novel secreted protein #150.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 68.5; DB 5; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1364
ID ABO34523 standard; protein; 548 AA.
DE Region of human secreted protein encoded by cDNA sequence #150.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOJ/) FLORENCE K A.
PA (OLSE/) OLSEN H S.

PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFU/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 5.7%; Score 68.5; DB 6; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1365
ID ADI23184 standard; protein; 548 AA.
DE Novel human secreted protein seq id 469.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOJ/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFU/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 5.7%; Score 68.5; DB 7; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1366
ID ADH17089 standard; protein; 548 AA.
DE Human translation initiation factor eIF3 p66 subunit protein.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGE-) SUGEN INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1367
ID ADH74186 standard; protein; 548 AA.
DE Human secreted protein #150.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.4e+02;
RESULT 1368
ID AAR58661 standard; protein; 552 AA.
DE Human PACAP receptor type 1-B2 protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 552;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1369
ID AAR58662 standard; protein; 553 AA.
DE Human PACAP receptor type 1C protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1370
ID AAR58660 standard; protein; 553 AA.
DE Human PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1371
ID ABB11705 standard; peptide; 588 AA.
DE Human GABA transporter homologue, SEQ ID NO:2075.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 588;
Best Local Similarity 19.6%; Pred. No. 1.5e+02;
RESULT 1372
ID ADP98892 standard; protein; 597 AA.
DE C. albicans specific gene, orf6.4254, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.7%; Score 68.5; DB 8; Length 597;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
RESULT 1373
ID ABU38306 standard; protein; 634 AA.
DE Protein encoded by Prokaryotic essential gene #23833.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 634;
Best Local Similarity 26.3%; Pred. No. 1.7e+02;
RESULT 1374
ID ABO81139 standard; protein; 660 AA.
DE Pseudomonas aeruginosa polypeptide #13314.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 660;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
RESULT 1375
ID AAG20246 standard; protein; 663 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22359.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 663;
Best Local Similarity 22.3%; Pred. No. 1.8e+02;
RESULT 1376
ID ABB53933 standard; protein; 670 AA.
DE Lactococcus lactis protein kup1.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.7%; Score 68.5; DB 5; Length 670;
Best Local Similarity 22.1%; Pred. No. 1.8e+02;
RESULT 1377
ID ABU50927 standard; protein; 691 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #270.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 5.7%; Score 68.5; DB 5; Length 691;
Best Local Similarity 19.2%; Pred. No. 1.9e+02;
RESULT 1378
ID AAG20245 standard; protein; 704 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22358.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 704;

Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1379
ID AAG20244 standard; protein; 724 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22357.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 724;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1380
ID AAU72535 standard; protein; 724 AA.
DE Arabidopsis cell cycle protein CCP25.
PN WO200185946-A2.
PD 15-NOV-2001.
PA (CROP-) CROPDISEIGN NV.
Query Match 5.7%; Score 68.5; DB 5; Length 724;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1381
ID ADC95469 standard; protein; 738 AA.
DE E. faecium protein sequence SEQ ID 5096.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 738;
Best Local Similarity 20.3%; Pred. No. 2.1e+02;
RESULT 1382
ID AAB46310 standard; protein; 788 AA.
DE H. pylori HPS115 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 5.7%; Score 68.5; DB 4; Length 788;
Best Local Similarity 19.2%; Pred. No. 2.3e+02;
RESULT 1383
ID AAY92103 standard; protein; 885 AA.
DE Human WFS1 mutant DEL508 YVILL.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOI/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 885;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1384
ID AAY92105 standard; protein; 890 AA.
DE Human WFS1 mutant G695V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOI/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1385
ID AAY92107 standard; protein; 890 AA.
DE Human WFS1 mutant P504L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOI/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1386
ID AAY92110 standard; protein; 890 AA.
DE Human WFS1 polymorphism I333V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.

PA (INOUE/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1387
ID AAY92109 standard; protein; 890 AA.
DE Human WFS1 polymorphism R456H.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOUE/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1388
ID AAY92100 standard; protein; 890 AA.
DE WFS1 polypeptide.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOUE/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1389
ID AAY92104 standard; protein; 890 AA.
DE Human WFS1 mutant P724L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOUE/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.7e+02;
RESULT 1390
ID ABP29861 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 8898.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.7e+02;
RESULT 1391
ID ABP28153 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 5482.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.7e+02;
RESULT 1392
ID AAY92102 standard; protein; 937 AA.
DE Human WFS1 mutant del82fs/ter937.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOUE/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 937;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1393
ID ADB70303 standard; protein; 1178 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3347.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 7; Length 1178;

Best Local Similarity 19.8%; Pred. No. 4e+02;
RESULT 1394
ID AAW88448 standard; protein; 1296 AA.
DE Caenorhabditis elegans NPC1 protein orthologue.
PN WO9901555-A1.
PD 14-JAN-1999.
PA (USSH) US DEPT HEALTH & HUMAN RESOURCES.
Query Match 5.7%; Score 68.5; DB 2; Length 1296;
Best Local Similarity 25.8%; Pred. No. 4.6e+02;
RESULT 1395
ID AAB30730 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone pH77CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;
Best Local Similarity 26.7%; Pred. No. 1.5e+03;
RESULT 1396
ID AAB30732 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;
Best Local Similarity 26.7%; Pred. No. 1.5e+03;
RESULT 1397
ID ADK16845 standard; protein; 200 AA.
DE Nanaorchaeum equitans cancer-associated (CA) protein #398.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.7%; Score 68; DB 8; Length 200;
Best Local Similarity 23.5%; Pred. No. 39;
RESULT 1398
ID AAB78946 standard; protein; 247 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:152.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 5.7%; Score 68; DB 4; Length 247;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1399
ID AAG91355 standard; protein; 247 AA.
DE C glutamicum protein fragment SEQ ID NO: 5109.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.7%; Score 68; DB 4; Length 247;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1400
ID AAY41212 standard; protein; 258 AA.
DE E. coli MtbB polypeptide.
PN WO9951753-A1.
PD 14-OCT-1999.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 68; DB 2; Length 258;
Best Local Similarity 23.0%; Pred. No. 56;
RESULT 1401
ID AAE21323 standard; protein; 273 AA.
DE Mouse MrgB10 (mas-related gene) protein.
PN WO200183555-A2.
PD 08-NOV-2001.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.7%; Score 68; DB 5; Length 273;
Best Local Similarity 26.1%; Pred. No. 60;
RESULT 1402
ID ADH08589 standard; protein; 273 AA.
DE MrgB10.
PN WO2004003133-A1.
PD 08-JAN-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.7%; Score 68; DB 8; Length 273;
Best Local Similarity 26.1%; Pred. No. 60;

RESULT 1403
ID ABU11963 standard; protein; 293 AA.
DE Human HGPBRMY11 C-terminal deletion mutant M1-G293.
PN WO200286123-A2.
PD 31-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 68; DB 6; Length 293;
Best Local Similarity 29.5%; Pred. No. 66;
RESULT 1404
ID AAG80106 standard; protein; 295 AA.
DE Human CCR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IPFP-) IPF PHARM GMBH.
PA (FORS-) FORSMANN U.
Query Match 5.7%; Score 68; DB 4; Length 295;
Best Local Similarity 26.0%; Pred. No. 67;
RESULT 1405
ID ADM05619 standard; protein; 295 AA.
DE Human protein of the invention SEQ ID NO:4304.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 68; DB 7; Length 295;
Best Local Similarity 28.3%; Pred. No. 67;
RESULT 1406
ID ABU11962 standard; protein; 308 AA.
DE Human HGPBRMY11 N-terminal deletion mutant E23-V330.
PN WO200286123-A2.
PD 31-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 68; DB 6; Length 308;
Best Local Similarity 29.5%; Pred. No. 71;
RESULT 1407
ID ADA35057 standard; protein; 309 AA.
DE Acinetobacter baumannii protein #2218.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68; DB 6; Length 309;
Best Local Similarity 20.6%; Pred. No. 72;
RESULT 1408
ID AAG17029 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17896.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68; DB 3; Length 330;
Best Local Similarity 21.5%; Pred. No. 78;
RESULT 1409
ID AAG42139 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52515.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68; DB 3; Length 330;
Best Local Similarity 21.5%; Pred. No. 78;
RESULT 1410
ID AAG77964 standard; protein; 330 AA.
DE Human G-protein coupled receptor PFI-017.
PN US2001039037-A1.
PD 08-NOV-2001.
PA (HARL-) HARLAND L.
Query Match 5.7%; Score 68; DB 5; Length 330;
Best Local Similarity 29.5%; Pred. No. 78;
RESULT 1411
ID ASU11900 standard; protein; 330 AA.
DE Human G-protein coupled receptor HGPBRMY11.
PN WO200286123-A2.
PD 31-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 68; DB 6; Length 330;
Best Local Similarity 29.5%; Pred. No. 78;
RESULT 1412
ID AAB85097 standard; protein; 331 AA.

DE Truncated cysLT2 cysteinyl leukotriene receptor (HG57).
PN WO200142269-A1.
PD 14-JUN-2001.
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
PA (ODOW/) O'DOWD B.
PA (GEOR/) GEORGE S R.
Query Match 5.7%; Score 68; DB 4; Length 331;
Best Local Similarity 29.5%; Pred. No. 79;
RESULT 1413
ID AAE07539 standard; protein; 341 AA.
DE Human G-protein coupled receptor 1b (GPCR1b) variant.
PN WO200159113-A2.
PD 16-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 68; DB 4; Length 341;
Best Local Similarity 29.5%; Pred. No. 82;
RESULT 1414
ID ASU11939 standard; protein; 341 AA.
DE Human G-protein coupled receptor HGPBRMY11v2.
PN WO200286123-A2.
PD 31-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 68; DB 6; Length 341;
Best Local Similarity 29.5%; Pred. No. 82;
RESULT 1415
ID ABP25610 standard; protein; 344 AA.
DE Streptococcus polypeptide SEQ ID NO 396.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68; DB 5; Length 344;
Best Local Similarity 20.2%; Pred. No. 83;
RESULT 1416
ID AAB73097 standard; protein; 346 AA.
DE Human LTC4 receptor SEQ ID NO: 2.
PN WO200119986-A1.
PD 22-MAR-2001.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (HELI-) HELIX RES INST.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1417
ID AAE07538 standard; protein; 346 AA.
DE Human G-protein coupled receptor 1a (GPCR1a) variant.
PN WO200159113-A2.
PD 16-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1418
ID AAU07294 standard; protein; 346 AA.
DE Cysteinyl leukotriene receptor HIPHUM00000007.
PN WO200159105-A1.
PD 16-AUG-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1419
ID AAB82852 standard; protein; 346 AA.
DE Human P2Y-like GPCR protein.
PN WO200168842-A2.
PD 20-SEP-2001.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1420
ID AAU04368 standard; protein; 346 AA.
DE Human G-protein coupled receptor, hRUP14.
PN WO200136471-A2.
PD 25-MAY-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68; DB 4; Length 346;

Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1421
ID AAU04383 standard; protein; 346 AA.
DE Human G-protein coupled receptor, hRUP14, mutant L246K.
PN WO200136471-A2.
PD 25-MAY-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1422
ID AAE08553 standard; protein; 346 AA.
DE Human G-protein coupled receptor (GPCR)-like protein.
PN WO200159118-A1.
PD 16-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1423
ID AAE12022 standard; protein; 346 AA.
DE Human G-protein coupled receptor, GCREC-1.
PN WO200172836-A2.
PD 04-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 68; DB 4; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1424
ID AAE17231 standard; protein; 346 AA.
DE Human CysLT2 GPCR (G-protein coupled receptor).
PN WO200192302-A2.
PD 08-DEC-2001.
PA (REG-) REGENERON PHARM INC.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1425
ID AAG77965 standard; protein; 346 AA.
DE Human G-protein coupled receptor PFI-017*.
PN US2001039037-A1.
PD 08-NOV-2001.
PA (HARL/) HARLAND L.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1426
ID ABP95624 standard; protein; 346 AA.
DE Human GPCR polypeptide SEQ ID NO 58.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1427
ID ABG66684 standard; protein; 346 AA.
DE Human novel polypeptide #19.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1428
ID ABB05229 standard; protein; 346 AA.
DE Human LTD4-like G-protein-coupled receptor protein SEQ ID NO:2.
PN WO200194580-A1.
PD 13-DEC-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1429
ID AAU10004 standard; protein; 346 AA.
DE Human CysLT2-like G-protein coupled receptor protein.
PN WO200177149-A2.
PD 18-OCT-2001.
PA (FARB-) BAYER AG.
Query Match 5.7%; Score 68; DB 5; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1430
ID ABU11923 standard; protein; 346 AA.
DE Human G-protein coupled receptor HGPBMV11v1.
PN WO200286123-A2.
PD 31-OCT-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 68; DB 6; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1431
ID ABP81707 standard; protein; 346 AA.
DE Human cysteinyl leukotriene CysLT2 receptor protein SEQ ID NO:589.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.7%; Score 68; DB 6; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1432
ID ADH00945 standard; protein; 346 AA.
DE Human cysteinyl leukotriene (CysLT2)-like GPCR protein.
PN US2003157541-A1.
PD 21-AUG-2003.
PA (FARB-) BAYER AG.
Query Match 5.7%; Score 68; DB 7; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1433
ID ADL96460 standard; protein; 346 AA.
DE Human G-protein-coupled receptor (GPCR) polypeptide #7.
PN US2003166148-A1.
PD 04-SEP-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LOWI/) LOWITZ K P.
Query Match 5.7%; Score 68; DB 7; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1434
ID ADL96534 standard; protein; 346 AA.
DE Human mutant G-protein-coupled receptor (GPCR) polypeptide #2.
PN US2003166148-A1.
PD 04-SEP-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LOWI/) LOWITZ K P.
Query Match 5.7%; Score 68; DB 7; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1435
ID ADK51004 standard; protein; 346 AA.
DE Human NOV6B protein sequence SeqID24.
PN WO2003083046-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 68; DB 7; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1436
ID ADK51002 standard; protein; 346 AA.
DE Human NOV6A protein sequence SeqID22.
PN WO2003083046-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 68; DB 7; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1437
ID ADG25220 standard; protein; 346 AA.
DE Human CysLT2 receptor.
PN US2003203833-A1.
PD 30-OCT-2003.
PA (IGNA/) IGNAR D M.
PA (PILL/) PILLAI S.
Query Match 5.7%; Score 68; DB 8; Length 346;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 1438
ID ADG25233 standard; protein; 346 AA.
DE Human CysLT2 receptor variant.
PN US2003203833-A1.

PD 30-OCT-2003.
PA (IGNA/) IGNAR D M.
PA (PILL/) PILLAI S.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 346;
RESULT 1439
ID ADH41891 standard; protein; 346 AA.
DE Novel human protein NOV35b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 346;
RESULT 1440
ID ADH41889 standard; protein; 346 AA.
DE Novel human protein NOV35a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 346;
RESULT 1441
ID ADO29277 standard; protein; 346 AA.
DE Human GPCR CVSLT2, SEQ ID NO:378.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 346;
RESULT 1442
ID AAB85094 standard; protein; 347 AA.
DE Human cysLT2 cysteinyl leukotriene receptor (HG57).
PN WO200142269-A1.
PD 14-JUN-2001.
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
PA (ODOW/) O'DOWD B.
PA (GEOR/) GEORGE S R.
Query Match
Best Local Similarity 5.7%; Score 68; DB 4; Length 347;
RESULT 1443
ID AAR52749 standard; protein; 355 AA.
DE C-C chemokine receptor.
PN WO9411504-A1.
PD 26-MAY-1994.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 2; Length 355;
RESULT 1444
ID AAW25751 standard; protein; 355 AA.
DE Human MIP-1alpha/RANTES receptor protein.
PN JP09176048-A.
PD 08-JUL-1997.
PA (TAKE-) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 5.7%; Score 68; DB 2; Length 355;
RESULT 1445
ID AAW26588 standard; protein; 355 AA.
DE Human MIP-1 alpha/RANTES receptor.
PN US652133-A.
PD 29-JUL-1997.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 5.7%; Score 68; DB 2; Length 355;
RESULT 1446
ID AAB20571 standard; protein; 355 AA.
DE Human CC-chemokine receptor 1 (CCR1) protein.
PN WO200044790-A1.
PD 03-AUG-2000.
PA (LEUK-) LEUKOSITE INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 3; Length 355;
RESULT 1447
ID ABU09082 standard; protein; 355 AA.

DE Human chemokine receptor-1 (CCR-1) polypeptide.
PN US2003018167-A1.
PD 23-JAN-2003.
PA (SCHE-) SCHERING CORP.
Query Match
Best Local Similarity 5.7%; Score 68; DB 6; Length 355;
RESULT 1448
ID ABP97724 standard; protein; 355 AA.
DE Amino acid sequence of human chemokine receptor CCR1.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPI-) TOPIGEN PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 6; Length 355;
RESULT 1449
ID ABP81790 standard; protein; 355 AA.
DE Human C-C chemokine receptor 1 protein SEQ ID NO:62.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 6; Length 355;
RESULT 1450
ID ADF76506 standard; protein; 355 AA.
DE Novel human secreted and transmembrane protein SeqID 180.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 7; Length 355;
RESULT 1451
ID ADO16838 standard; protein; 355 AA.
DE CCR1 amino acid sequence.
PN WO2003047420-A2.
PD 12-JUN-2003.
PA (CHEM-) CHEMOCENTRYX INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 7; Length 355;
RESULT 1452
ID ADO29219 standard; protein; 355 AA.
DE Human GPCR CCR1, SEQ ID NO:320.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 355;
RESULT 1453
ID ADO19490 standard; protein; 355 AA.
DE Human PRO polypeptide #210.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 355;
RESULT 1454
ID ADO19492 standard; protein; 355 AA.
DE Human PRO polypeptide #211.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 355;
RESULT 1455
ID ADO21524 standard; protein; 355 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4344.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 355;
RESULT 1456
ID ADP88568 standard; protein; 355 AA.
DE Human chemokine (C-C) motif receptor 1 CCR1.

PN WO2004052186-A2.
PD 24-JUN-2004.
PA (FORS-) FORSYTH INST. 5.7%; Score 68; DB 8; Length 355;
Query Match
Best Local Similarity 26.0%; Pred. No. 87;
RESULT 1457
ID ADP88570 standard; protein; 355 AA.
DE Human macrophage inflammatory protein-1-alpha/RANTES receptor.
PN WO2004052186-A2.
PD 24-JUN-2004.
PA (FORS-) FORSYTH INST. 5.7%; Score 68; DB 8; Length 355;
Query Match
Best Local Similarity 26.0%; Pred. No. 87;
RESULT 1458
ID ABU44640 standard; protein; 357 AA.
DE Protein encoded by Prokaryotic essential gene #30167.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.7%; Score 68; DB 6; Length 357;
Query Match
Best Local Similarity 23.5%; Pred. No. 87;
RESULT 1459
ID ADD46815 standard; protein; 365 AA.
DE Rat Protein BAA03912, SEQ ID NO 12501.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 5.7%; Score 68; DB 7; Length 365;
Best Local Similarity 21.8%; Pred. No. 90;
RESULT 1460
ID ADD46813 standard; protein; 365 AA.
DE Rat Protein BAA03912, SEQ ID NO 12499.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 5.7%; Score 68; DB 7; Length 365;
Best Local Similarity 21.8%; Pred. No. 90;
RESULT 1461
ID AB58017 standard; protein; 372 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 843.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 5.7%; Score 68; DB 4; Length 372;
Best Local Similarity 21.1%; Pred. No. 93;
RESULT 1462
ID ADC97421 standard; protein; 373 AA.
DE E. faecium protein sequence SEQ ID 7048.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 5.7%; Score 68; DB 7; Length 373;
Best Local Similarity 22.4%; Pred. No. 93;
RESULT 1463
ID ADN47559 standard; protein; 399 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1437.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 5.7%; Score 68; DB 8; Length 389;
Best Local Similarity 21.8%; Pred. No. 98;
RESULT 1464
ID ABU50321 standard; protein; 393 AA.
DE Protein encoded by Prokaryotic essential gene #35848.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.7%; Score 68; DB 6; Length 393;
Query Match
Best Local Similarity 21.6%; Pred. No. 1e+02;
RESULT 1465
ID ABU31520 standard; protein; 395 AA.

DE Protein encoded by Prokaryotic essential gene #17047.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.7%; Score 68; DB 6; Length 395;
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+02;
RESULT 1466
ID ABU22337 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #7864.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.7%; Score 68; DB 6; Length 396;
Query Match
Best Local Similarity 21.1%; Pred. No. 1e+02;
RESULT 1467
ID ABO64352 standard; protein; 414 AA.
DE Klebsiella pneumoniae polypeptide seqid 10869.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 5.7%; Score 68; DB 7; Length 414;
Query Match
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1468
ID AAY05501 standard; protein; 426 AA.
DE Bacillus subtilis metalloprotease YHFN.
PN WO9914341-A2.
PD 25-MAR-1999.
PA (GEMV) GENENCOR INT INC.
PA (GEMV) GENENCOR INT BV.
Query Match
Best Local Similarity 5.7%; Score 68; DB 2; Length 426;
Best Local Similarity 21.2%; Pred. No. 1.1e+02;
RESULT 1469
ID ABB64152 standard; protein; 426 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19248.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 5.7%; Score 68; DB 4; Length 426;
Query Match
Best Local Similarity 24.0%; Pred. No. 1.1e+02;
RESULT 1470
ID AAY99670 standard; protein; 446 AA.
DE Human GTPase associated protein-21.
PN WO200031263-A2.
PD 02-JUN-2000.
PA (INCY-) INCYTE PHARM INC. 5.7%; Score 68; DB 3; Length 446;
Query Match
Best Local Similarity 27.4%; Pred. No. 1.2e+02;
RESULT 1471
ID AAM39368 standard; protein; 446 AA.
DE Human polypeptide SEQ ID NO 2513.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 5.7%; Score 68; DB 4; Length 446;
Query Match
Best Local Similarity 27.4%; Pred. No. 1.2e+02;
RESULT 1472
ID ABUS2686 standard; protein; 446 AA.
DE Human signal transduction-associated protein from DKF2phfbr2_2c17.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT. 5.7%; Score 68; DB 4; Length 446;
Query Match
Best Local Similarity 27.4%; Pred. No. 1.2e+02;
RESULT 1473
ID ABP60125 standard; protein; 450 AA.
DE Human epilepsy related protein 49.50.
PN CN1345812-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC. 5.7%; Score 68; DB 5; Length 450;
Query Match
Best Local Similarity 28.3%; Pred. No. 1.2e+02;
RESULT 1474
ID AAR67692 standard; protein; 471 AA.

DE C. albicans caaur1 gene product.
PN AU9463129-A.
PD 01-DEC-1994.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 5.7%; Score 68; DB 2; Length 471;
Best Local Similarity 25.4%; Pred. No. 1.3e+02;
RESULT 1475
ID AAR88133 standard; protein; 471 AA.
DE Aureobasidin sensitivity regulatory gene caaur1 product.
PN EP692534-A2.
PD 17-JAN-1996.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 5.7%; Score 68; DB 2; Length 471;
Best Local Similarity 25.4%; Pred. No. 1.3e+02;
RESULT 1476
ID AAU15078 standard; protein; 471 AA.
DE Protein encoded by C. albicans essential gene CayKL004W (AUR1).
PN W0200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68; DB 4; Length 471;
Best Local Similarity 25.4%; Pred. No. 1.3e+02;
RESULT 1477
ID ABP73191 standard; protein; 471 AA.
DE Candida albicans essential protein SEQ ID NO 7028.
PN W0200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68; DB 5; Length 471;
Best Local Similarity 25.4%; Pred. No. 1.3e+02;
RESULT 1478
ID AAR67696 standard; protein; 472 AA.
DE C. albicans caaur1 gene product.
PN AU9463129-A.
PD 01-DEC-1994.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 5.7%; Score 68; DB 2; Length 472;
Best Local Similarity 25.4%; Pred. No. 1.3e+02;
RESULT 1479
ID AAU39938 standard; protein; 472 AA.
DE Propionibacterium acnes immunogenic protein #834.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 68; DB 4; Length 472;
Best Local Similarity 19.4%; Pred. No. 1.3e+02;
RESULT 1480
ID AAM36457 standard; protein; 472 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1133.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 68; DB 6; Length 472;
Best Local Similarity 19.4%; Pred. No. 1.3e+02;
RESULT 1481
ID AAM41154 standard; protein; 485 AA.
DE Human polypeptide SEQ ID NO 6085.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68; DB 4; Length 485;
Best Local Similarity 27.4%; Pred. No. 1.3e+02;
RESULT 1482
ID AAW02271 standard; protein; 488 AA.
DE Human prostaglandin receptor EP2.
PN W09508664-A1.
PD 09-MAR-1995.
PA (MERI) MERCK PROSST CANADA INC.
Query Match 5.7%; Score 68; DB 2; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1483
ID ABB56384 standard; protein; 488 AA.
DE Non-endogenous human GPCR protein, SEQ ID NO: 561.

PN W0200177172-A2.
PD 18-OCT-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68; DB 4; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1484
ID ABP81905 standard; protein; 488 AA.
DE Human prostaglandin E receptor EP4 protein SEQ ID NO:296.
PN W0200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.7%; Score 68; DB 6; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1485
ID AAO30984 standard; protein; 488 AA.
DE Human prostaglandin E receptor (EP4) protein.
PN W02003051180-A2.
PD 26-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68; DB 6; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1486
ID ADN40008 standard; protein; 488 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C378.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.7%; Score 68; DB 7; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1487
ID ADO29622 standard; protein; 488 AA.
DE Human GPCR PTGER4, SEQ ID NO:724.
PN W02004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 68; DB 8; Length 488;
Best Local Similarity 26.8%; Pred. No. 1.3e+02;
RESULT 1488
ID ABG26292 standard; protein; 490 AA.
DE Novel human diagnostic protein #26283.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68; DB 4; Length 490;
Best Local Similarity 26.8%; Pred. No. 1.4e+02;
RESULT 1489
ID ABR57071 standard; protein; 490 AA.
DE Baboon/macaque prostaglandin E2 receptor EP4 protein SEQ ID NO:3.
PN EP1293512-A2.
PD 19-MAR-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 5.7%; Score 68; DB 6; Length 490;
Best Local Similarity 26.8%; Pred. No. 1.4e+02;
RESULT 1490
ID ADH11546 standard; protein; 490 AA.
DE Chimpanzee prostaglandin E2 receptor EP4 subtype, SEQ ID 2.
PN EP1295897-A1.
PD 26-MAR-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 5.7%; Score 68; DB 7; Length 490;
Best Local Similarity 26.8%; Pred. No. 1.4e+02;
RESULT 1491
ID AAW70285 standard; protein; 519 AA.
DE Oryza sativa RNA polymerase sigma factor.
PN JP10201475-A.
PD 04-AUG-1998.
PA (HOKK) HOKKO CHEM IND CO LTD.
Query Match 5.7%; Score 68; DB 2; Length 519;
Best Local Similarity 24.1%; Pred. No. 1.5e+02;
RESULT 1492
ID ABU37983 standard; protein; 542 AA.
DE Protein encoded by prokaryotic essential gene #23510.

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PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.7%; Score 68; DB 6; Length 542;
 Best Local Similarity 30.6%; Pred. No. 1.6e+02;
 RESULT 1493
 ID ADF08283 standard; protein; 542 AA.
 DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 116.
 PN WO2004046177-A2.
 PD 03-JUN-2004.
 PA (CHIR) CHIRON SRL.
 Query Match 5.7%; Score 68; DB 8; Length 542;
 Best Local Similarity 30.6%; Pred. No. 1.6e+02;
 RESULT 1494
 ID AAU72914 standard; protein; 562 AA.
 DE Neisseria meningitidis virulence protein #4.
 PN WO200185772-A2.
 PD 15-NOV-2001.
 PA (MICR-) MICROSCIENCE LTD.
 Query Match 5.7%; Score 68; DB 5; Length 562;
 Best Local Similarity 30.6%; Pred. No. 1.6e+02;
 RESULT 1495
 ID AAU72948 standard; protein; 562 AA.
 DE Neisseria meningitidis virulence protein #38.
 PN WO200185772-A2.
 PD 15-NOV-2001.
 PA (MICR-) MICROSCIENCE LTD.
 Query Match 5.7%; Score 68; DB 5; Length 562;
 Best Local Similarity 30.6%; Pred. No. 1.6e+02;
 RESULT 1496
 ID AAU72956 standard; protein; 562 AA.
 DE Neisseria meningitidis virulence protein #46.
 PN WO200185772-A2.
 PD 15-NOV-2001.
 PA (MICR-) MICROSCIENCE LTD.
 Query Match 5.7%; Score 68; DB 5; Length 562;
 Best Local Similarity 30.6%; Pred. No. 1.6e+02;
 RESULT 1497
 ID AAE28968 standard; protein; 646 AA.
 DE Human ABCG4 transporter protein #2.
 PN WO200270691-A2.
 PD 12-SEP-2002.
 PA (ACTI-) ACTIVE PASS PHARM INC.
 Query Match 5.7%; Score 68; DB 5; Length 646;
 Best Local Similarity 22.3%; Pred. No. 2e+02;
 RESULT 1498
 ID ABB92106 standard; protein; 664 AA.
 DE Herbicidally active polypeptide SEQ ID NO 1317.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 5.7%; Score 68; DB 5; Length 664;
 Best Local Similarity 19.3%; Pred. No. 2.1e+02;
 RESULT 1499
 ID ABB71668 standard; protein; 714 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 41796.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.7%; Score 68; DB 4; Length 714;
 Best Local Similarity 28.4%; Pred. No. 2.3e+02;
 RESULT 1500
 ID ABA41819 standard; protein; 717 AA.
 DE Human ORFX ORF1583 polypeptide sequence SEQ ID NO:3166.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.7%; Score 68; DB 3; Length 717;
 Best Local Similarity 28.3%; Pred. No. 2.3e+02;